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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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SUMMARIES

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RESULT 1 AX511567	
LOCUS	AX511567 188 bp DNA linear PAT 27-SEP-2002
DEFINITION	9.
ACCESSION	AX511567
VERSION	AX511567.1 GI:23392406
KEYWORDS	
SOURCE	Potato virus X
ORGANISM	Potato virus X
	Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
REFERENCE	
AUTHORS	Santa-Cruz, S., Pogue, G.P., Toth, R.L., Chapman, S. and Carr, F.
TITLE	Expression of foreign genes from plant virus vectors
JOURNAL	Patent: WO 02055719-A 1 18-JUL-2002;
	BIOSOURCE GENETICS CORPORATION (115)

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Expression of foreign genes from plant
Patent: WO 02055719-A 5 18-UL-2002;
BIOSOURCE GENETICS CORPORATION (US)
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Sequence 5 from Patent WOO2055719.
AX511571
AX511571.1 GI:23392410
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/mol_type="genomic DNA"
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                                                                GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 142918] from the original journal article. This sequence comes from Fig. 2.

Location/Qualifiers
                                                                                                                                                                                                          Tobamovirus of cruciferous plants: nucleotide sequence of genes of the transport protein, capsid protein, and 3'-terminal untranslated
                                                                                                                                                                         Dokl. Akad. Nauk. 332 (4), 518-522 (1993)
                                                                                                                                                                                                                                                                                     Viruses; ssRNA positive-strand viruses, no 1 (bases 1 to 1537)
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Dorokhov, Iu.L., Ivanov, P.A.,
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/db_xref="taxon:12183"
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Pred. No. 1.2e-33;
D; Mismatches 10
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                                           5'-untranslated region and nonstructural protein genes controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                6312 bp
Tobacco mosaic virus (Crucifer)
polymerase; 122K protein; trans-
Z29370
                                  replication viral
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                                                                                                                                                                                                                                                                                                 Truses; ssRNA positive strand viruses, no DNA stage; Tobamovirus (bases 1 to 6311)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGTACAGACCGGAGAAGTACGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAA 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kl. Akad. Nauk SSSR 332, 518-522 (1993)
(bases 1 to 6312)
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VRQQFSNLLSAVVAPSQRFPEGGSRVYVNSAVIKPLYEALMKSFDTRNRIIETEBESR
PSASBVLTRHNVLMMRBFPLEVKFSCC" 1 others
274 c 406 g 433 t 1 others
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ESETLCDIDLLINVPLDKYRYVGILGAVFTGEWLVPDFVKGGVTISVIDKRLANSKEC
VIGTYRAAAKSKRFQFKLVPNYFVSTVDAKRKPWQVHVRIQDLKIEAGWQPLALEVVS
VAMVTNNVVHKGLREKVVAINDPDVEGFEGVVDEFVDSVAAFKAVDNFKRRKKKVEEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="capsid protein"
/protein_id="AAB29320.1"
/db_xref="GI:544602"
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/protein_id="AAB29319.1"
/db_xref="GI:544601"
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93.7%;
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1219
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      792-798 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                             RNA helicase; RNA-dependent RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morozov, S.Tu., Etimov, V.A., Novikov, V.K., Agranovsky, A.A., Complete nucleotide sequence and genome organization of a tobamovirus infecting cruciferae plants PEBS Lett. 350 (1), 5-8 (1994) 94341777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dorokhov,Y.
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                                                                                          RNA-helicase
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VTTFIGNTIIIAACLSSMIPMDKVIKAAFCGDDSLIYIPKGLDLPDIQAGANLMWNFE
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SLTYDIGGNESAHLFKGRDYVHCCMPNLDVRDIARHEGHKEAIHSYVNRLKRQQRPVP
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HEVQGETYEKTAIVRLTSTPLEIISRASPHVLVALTRHTTRCKYYTVVLDPMVNVISE
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DMGKLKTLTTCSPNGEPPEPNAKVILVDGVPGCGKTKEIIEKVNFSEDLILVPGKEAS
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VNKDFVYTVLNHIKTYQAKALTYANVLSFVESIRSRVIINGVTARSEWDTDKAILGPL
/product="122K"
/protein_id="CAA82558.1"
                                                                                                                                                                                                                                                                                                                                 MEKLSNFLLDMYRVEAGIQXQLQIDAVFKGTNLFVQTPKSGDWRDMQFYNDTLLPGNS
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/product="178K"
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                                                                                                        function="protein containing methyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                       )CDVAYVYGDTQQIPFICRVANFPYPAHFAKLVADEKEVRRVTLRCPADVTYFLNKKY
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/translation-"MAQFQQTIDMQTLQAAAGPNSLYNDLASRRYYDNAVEELNARSR
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/db_xref="GI:619908"
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/mol_type="genomic RNA"
/db_xref="taxon:12242"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KYVCKTFFPASQRFVYHKEFLVTRVNTWYCKFTRVDTFTLFRGVYHNNVDCEEFYKP
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AX511572
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KEYWORDS
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Best Local
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                 AX511572 180 bp
Sequence 6 from Patent WO02055719.
AX511572
AX511572.1 GI:23392411
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                                                                                                                                                                                                                                   AAGTACAGACCGGAGAAGTACGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAA 175
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MDAMHYKKTLAMINAERT IFKONAALNFWFPKVRDMYIVPLEDAS ITTGRWSRREYM
VNKDFVTSVLHHIKTYGAKALTY ANVLSFVESI RSRV II NGVTARSEMDTDKAILGPL
AMTFFLITKLGHVQDEIILKKFOKFDRTNELLWTSLCDALMGVI PSWETLYRGGFV
KVAEQALEIK IPELYCTFADRLVLQXKKAEEFOSCDLSKPLEBESKYYNALSELSVLE
NLDSFDLEAFKTLCGOKSVDPDMAAKVVVAINKCELTLPFKKPTEELISESLKTGEGT
SAEHKDVLSLQNDAPFFCVKNLVEGSVPAYGMCFXGGGFDKLDVDIADFHLKSVDAVK
RGTMMSAVTTGSIEVROMKNYIDYLSAASIARTVSAICKVLRDVHGVDPESOEKSGVWD
VRRGRWLLKPNAKSHAMGVAEDANHKLJTVLLNWDDGKPCDETWFRVAVSSDELIYG
SMGKLKTLTTCSFNGEPPEPNAKVILVDGVPGGGKTKEIIEKVNFSEDLILVPGKEAS
MKKLKTLTTCSFNGEPPEPNAKVILVDGVPGGKTKEIIEKVNFSEDLILVPGKEAS
KMIIRRANHAGYIRADKDNYSTYDSFLMHPSRRVFKLFIDEGLMLHTGCVWELLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSYNITNENGYGYFAAVWAEPIPMLNGCISALSGSYGTGAARDT VRQQFSNLLGAVVABSGRFPETGSRVTVNSAVIKPLYEALMKSFDTRNRIIETEEESR PSASEVRNATGRVDATVSIRSGIGLLLSELSSGHGYMNRAEFEALVPWTTAAAT" 1213 c 1590 g 1709 t
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/translation="MSIVSYEPKVSDFLNLSKKEEILPKALTRLKTVSISTKDIISVK
ESETLCDIDLLINVPLDKYRYVGILGAVFTGEWLVPDEVKGGVTISVIDKRLANSKEC
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DGAVMCTSAVERSVKAEVVRGKGALNPITLPLEGKILTFTQADKFELLEKGYKDVNTV
HEVQGETYEKTAIVRLTSTPLEIISRASPHVLVALTRHTTRCKYYTVVLDPMVNVISE
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VAMVTNNVVMKGLREKVVAINDPDVEGFEGVVDEFVDSVAAFKAVDNFKRRKKVEEK
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RPKVHFSKAVSTEQTLIATNAYPEFEISFTHTQSAVHSLAGGFRSLELEYLMMQVPFG
SLTYDIGGNFSAHLFKGRDYVHCCMPNLDVRDIARHEGHKEAIHSYVNRLKRQQRPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="coat protein"
/note="ORF4"
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/db_xref="GI:488716"
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/note="ORF3"
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'db_xref="GI:488715"
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/db_xref="SPTREMBL:Q88603"
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Expression of foreign genes from plant
Patent: WO 02055719-A 3 18-JUL-2002;
BIOSOURCE GENETICS CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                            187 bp
Sequence 3 from Patent WOO2055719.
AX511569
                                                                                                                                                                                                                                                                                                                                            Potato virus X Potato virus X
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Potato virus
                                                                                                                                       Similarity
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                                                                     AATTCGTCGATTCGGTTGCAGCATTTAAAGCGGTTGACAACTTTAAAAGAAGGAAAAAGA 121
                                                                                     AATTCGTCGATTCGGTTGCAGCATTTAAAGCGGTTGACAACTTTAAAAGAAGAAGGAAAAAGA 88
CTGATTCGTTTAATTTGAAAGAAGAAGAAGAGCTCACCAT 186
                       AGGTTGAAGAAAAGGGTGTAGTAAGTAAGTACAGACCGGAGAAGTACGCCGGTC
                                AGGTTGAAGAAAAGGGTGTAGTAAGTAATAAGTACAGACCGGAGAAGTACGCCGGTC 148
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                                                                                                                                                                                    /organism="Potato virus
/mol_type="genomic DNA"
/db_xref="taxon:12183"
47 c 27 g
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/mol_type="genomic DNA"
/db_xref="taxon:12183"
31 c 52 g 3
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                                                                                                                        Score 150; DB 6;
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Pred. No. 5.1e-3
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                                                                                                                                                                                                                                                                                                                               no DNA stage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 GAAGGTTGAAGAAAAGGGTGTAGTAAGTAAGTATAAGTACAGACCGGAGAAGTACGCCGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
             Submitted (09-NOV-1993) Biochemistry & Molecular Biology, Oklahoma State University, NRC 246, Stillwater, OK 74078-0454, USA 4 (bases 1 to 6311)
                                                                                                                                       2 (bases 1 to 67; 3392 to 6311)
Lartey,R.T., Voss,T.C. and Melcher,U.K.
Completion of a cDNA sequence from a tobamovirus
                                                                                                                                                                                                                  vein-clearing virus
Arch. Virol. 138 (3-4), 287-298 (1994)
                                                                                                                                                                                                                                                                                                                            Turnip vein-clearing virus
Turnip vein-clearing virus
                                                                                                                                                                                                                                                                                                                                                                                           Turnip vein-clearing U03387 L22518
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Location/Qualifiers
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Sequence 2 from Patent W002055719,
AX511568
AX511568.1 GI:23392407
                                                                                                                                                                                                                                                                                                                                                                            U03387.1 GI:2894629
                                                                Direct Submission
                                                                                                                                                                                                                                                           Electron microscopic and molecular characterization of turnip
                                                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
1 (bases 68 to 3391)
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Potato virus X
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                                                                                          e 166, 321-322 (1995)
(bases 1 to 6311)
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/db_xref="taxon:12183"
51 c 76 g
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                                                                                                                                                                                                                                                                            ., Lane, L.C.
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Submitted (18-FEB-1998) Biochemistry & Molecular Biology,
State University, NRC 246, Stillwater, OK 74078-0454, USA
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/product="RNA replicase component"
/protein_id="AAC02782.1"
                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                            MEKLSNFLLDMYRVEAGVQYQLQIDAVFRDSNLFVQTPKSGDWRDMQFYYDALLPGNS
PILNEFDAVTMNLRDISLNVKDCRIDFSKSVQLPKEQPIFLKPKIRTAAEMPRTAGLL
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RPKVHFSKAVSTEQTLIATNAYPEFEISFTHTQSAVHSLAGGLRSLELEYLMMQVPFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Turnip vein-clearing virus"
/mol_type="genomic RNA"
/strain="OSU"
                                                                                                                        'note="contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEVQGETYEKTAIVRLTSTPLEIISSASPHVLVALTRHTTCCKYYTVVLDPMVNVISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="RNA replicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTMMSAVYTGSIKVQQMKNYIDYLSASLAATVSNLCKVLRDVHGVDPESQEKSGVWD
RRGRWLLKPNAKSHAWGVAEDANHKLVIVLLNWDDGKPVCDETWFRVAVSSD$LIYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAC02783.1"
/db_xref="GI:619645"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note-"contains RNA polymerase; stop codon at 3389. is suppressed under certain conditions and expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /specific_host="Brassica rapa"
/db_xref="taxon:29272"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update by submitter
1998 this sequence version replaced g1:619581
ocation/Qualifiers
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                                                                                                               capping methyltransferase
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/translation="MAGFQQTIDMQTLQAAAGRNSLVNDLASRRVYDNAVEELNARSR
/translation="MAGFQQTIDMQTLQAAAGRNSLVNDLASRRVYDNAVEELNARSR
RPKYHFSKAVSTEQTLIATNAYPEFETSFTHYOSAVHSLAGGLRSLELEYLMMQVPFG
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EYORAAFNNYAENPHEVHCOKPFQCELTTAYGTDYKAVALHSIYDIPVEEFGSALLR
KNVKKTCFAAFHFHENMLLDCDTVTLDEIGATFQKSGDNLSFFFHNESTLNYTHSFSNI
IKYYCKTFFPASQRFVYHKEFLVTRAVTHYXCKFTNDTFTLFRGVYHNVDCEEFYKA
MDDAMHYKKTLAMLNAERTIFKDNAALLFHFFFKVDTUVIVLFDASITTGRMSRREIM
VNKDFVYTULHIKTYQAKALTYANVLSFVESIRSRVIINGVTARSEMDTDKALIGFL
AMTFFLITKLGHVQDEIILKKFQKFDRTTNELIWTSLCDALMGVIPSVKETLVRGGFV
KVAEQALEIRVPELYCTFADRLVLQYKKAEFFQSCDLSKPLEESEKYYNALSELSVLE
NLDSFDLEAFKTLCQQKNUDDDAAKVVYAIMKSELTLPFKKPTEBEISESLKPGEGS
CAEHKEVLSLQNDAFFPCVKNLVEGSVPAYGNCFKGGFDKLDVDLAGDFHLKSVDAVK
KGEMSAVYTGSIKYQQMKNYIDYLSASLAATVSNLCKVLRDVHGUDPESQEKSGVMD

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ORGANISM
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KEYWORDS
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AB003936
FEATURES
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                                                                                                                                                                                                                               Shimamoto, I., Sonoda, S., Vazquez, P., Minaka, N. and Nishiguchi, M. Nucleotide sequence analysis of the 3' terminal region of a wasabi strain of crucifer tobamovirus genomic RNA: subgrouping of crucifer
                                                                                                                                                                                                                                                                                                                                                         protein;
Crucifer
                                                                                                                                                                                                                                                                                                                                                                     AB003936.1 GI:3242449
RNA replicase read through component;
protein; replicase.
                           Agrobiological Resources, Department of Molecular Biology; Kannonndai 2-1-2, Tsukuba, Ibaraki 305, Japan (E-mail:mnishigu@ss.abr.affrc.go.jp, Tel:81-298-38-7005,
             (E-mail:mnishigu@ss.abr.affrc.
Fax:81-298-38-7408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crucifer
                                                                                Submitted (15-MAY-1997) Masamichi Nishiguchi, National Institute
                                                                                                                                                                                                    Arch. Virol.
                                                                                                                             Nishiguchi, M.
                                                                                                                                                                                                                       tobamoviruses
                                                                                                                                                                                                                                                                                                                        Viruses;
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tobamovirus genomic
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/protein_id="AACO2785.1"
/protein_id="AACO2785.1"
/db_xref="Ci:514839"
/translation="MSYNITNPNQYQYFAAVWAEPIPHLNQCHSALSQSYQTQAARDT
/translation="MSYNITNPNQYQYFAAVWAEPIPHLNQCHSALSQSYQTQAARDT
/TRANSLESHVANATQRYDATAAIRSQIQLLLSELSNGHGYMNRAEFEALLPWTTAPAT"
1195 c 1586 g 1720 t
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QCDVALYVGDTKQIPFICRVANPPYAHFAKLYADEKEVRKYLLEGPADVTYFLNKKY
DGAVWCTSAVERSVKAEVVRGKGALMPITLPLEGKILTFDADKFELLEKGYKDVTVH
HEVQGETYEKTAIVRLTSTPLEIISSASPHVLVALTRHTTCCKYYTVVLDPMVNVISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="movement protein"
/protein_id="AAC02784.1"
/db_xref="GI:514838"
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                                                                                                                                                                                                  143 (9), 1801-1813 (1998)
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Pred. No. 1.7e-26;
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AB017504
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Crucifer tobamovirus genomic
AB017504
AB017504.1 GI:18146768
  Nucleotide sequence
strain of crucufer t
                Shimamoto, I., Sonoda, S., Vazquez, P., Nucleotide sequence analysis of the
                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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RMLLERVDTSKELFYTRKTF7QIEEFFSDLDSSQAIEILELDVSKYDKSQNEFHCAVE
YKIWEKLGIDEWLAFWMGGHRKTILKDYTAGIKTCLMYQRKSGDVTFFIGNTIIJA
CLSSMIPMEKVIKAAFCGDDSLIYIPKGLDLPDIQAGANLTWNEEAKLFRKKYGYLCG
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vrqqfsnllsaivtpnqrfpetgyrvyvnsavlkplyealmksfdtrnriieteeesr
psasevanatqrvddatvairsqiqlllselssghglmnraefevlipmatapak"
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ESESLCDIDLLVNVPLDKFRYVGILGVVFTGEWLIPDFVKGGVTVSVIDKRLENSKEC
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/protein_id="BAA28951.1"
/db_xref="GI:3242452"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVISKYKYRPEKYAGPDSLLNKEENVIQHHELESVPVFRSGMGGAHSNA'
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VAMVTNNVVVKGLRERVIAVDDPNVEGFEGVVDEFIDSVAAFKAVDNFRKKKKKIGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="movement protein"
/protein_id="BAA28950.1"
/db_xref="GI:3242451"
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/strain="wasabi"
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/protein_id="BAA28949.1"
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tobamovirus genomic RNA: subgrouping of crucifer
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Pred. No. 2.3e-2
0; Mismatches
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                                                                                                                                                                                          RNA
complete
                  Minaka, N. and Nishiguchi, M. 3' terminal region of a wasa
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genome,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee, K., Nishiguchi, M. and Kashiwazaki, S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tobamoviruses
Arch. Virol. (1998) In press
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KLAEESLEIKIPELYCTFTDRLVLEYKRAEEFKSCDLSKPLEESEKYYNALSELSVLE
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EYQRAAFNNYSENPHFYHCDQPFQQCALSTYNGDDTYAVALHSIYDIPVEEFGGALLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESSTYGQLADFNFYDLPAYDEYKHMIKSQPKQKLDLSIQDEYPALQTIYYHSKKINAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GETYEKTAIVRLTATPLEIISRASPHVLVALTRHTTSCKYFTYVLDPLYSVISEMEKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLDSFDLEAFKELCQKKSVDPDVAAKVVVAIMKSELTLDFKKPTEEEIAESLSNDTTR
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RYVYGDTQQIPFICRVANFFYFKHFARLVVDEKEDRRITLRCPADVTFFLNKKYDGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGNTIIIAACLSSMIPMEKVIKAAFCGDDSLIYIPKGLDLPDIQAGANLTWNFEAKLF
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VNKDEVYTVLNHIKTYQAKALTYANVLSEVESIRSRVIINGVTARSEWDTDKAILGEL
AMTEELVTKLGHVQDEIVLKKEQKEDSTAKELLWTSLCDALMGYIPSVKETLARGGEV
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IKYYCKTFFPASQRFYYHKEFLVTRVNTWYCKFTRVDTFTLFRGYYKNSVDSDEFYKA
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SLTYDIGGNFAAHLFKGRDYVHCCMPNLDVRDIARHEGHKEAVFGYISRLKRQRRPVP
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66. .4859
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                                                             Research Center, Department of Plant Protection; 3-1-1 Kannondai, Tsukuba, Ibaraki 305-8666, Japan (E-mail:skashiwa@narc.affrc.go.jp, Tel:81-298-38-8932)
Location/Onalifican
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Lee, K., Nishiguchi, M. and Kashiwazaki, S.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crucifer tobamovirus
                                                                                                                                                                                                                                                                 Complete nucleotide
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                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                              tobamovirus
                                                                                                                                                                                                                                                               Lee,K., Nishiguchi,M. and Kashiwazaki,S.
Complete nucleotide sequences of two isolates
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VAMYINNVVKGLRERVIAVDDPNVEGFEGVVDFFRSGMGGAHSNA"
                                                           Location/Qualifiers
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LCTSSYERSVSAQVVRGKGALNPITLPLEGKILTFTQADKFELLDKGYKDVNTVHEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSAYYTGNIKYQQMKNFYDYLSASLSATYSNLCKYLRDYHGYDPESQEKSGYMDYRRE
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LKTLTSCCYDGEPPEPKAKYYLVDGYPGCGKTKEILEKYNFSEDLYLYPGKEASKMII
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genomic RNA,
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Pred. No. 2.3e-21;
D; Mismatches 35
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complete
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NLOSFDLEAFKELCQKKSVDPDVAAKVVVAINKSELTLPFKKPTEEE I AESLSNDT I R
NEGLSLSNTAFFFCYSNLEGGLVFAGGLCPKGGGFDKI DMDI SEFHLRSVDAVKKGAM
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AMIKRNNNAPPLITGTIDIEDTASLVVEKFWDSYIVKEFSGIEGMAKTREGFSRWLSKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPKYHFSKSYSTEGTILLASNAYPEFEISFTHTQHAVHSLAGGLRSLELEYLMMQVPFG
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KNVKVCYAAFHFHENMLLDCDTVTLEEIGATFQRAGDKLNFFFHNESTLNYTHSFSNI
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NCAYFSQLDEAVAEVHKTAVGGSFAYCSIIKYLSDKRLFKDLFFV*
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MSAVYTGNIKVQQMKNFVDYLSASLSATVSNLCKVLRDVHGVDPESQEKSGVPDVTRG
RWLLKPNAKCHAWGVAEDANHKLYIVLLNWDDGKPVCDQTWYRLAVSSDSLVYSDMGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNKDFVYTVLNHIKTYQAKALTYANVLSFVESIRSRVIINGVTARSEWDTDKAILGPL
AMTFFPVTKLGHVQDEIVLKKFOKFDSTAKELIWTSLCDALMGVIPSVKETLARGGFV
KLAEESLEIKIPELYCTFTDRLVLEYKKAEEFKSCDLSKPLEESEKYYNALSELSVLE
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IKYVCKTFFPASQRFVYHKEFLVTRVNTWYCKFTRVDTFTLFRGVYKNSVDSDEFYKA
MDDAWEYKKTLAMLNAERT I FKDNAA I NEWFPKCRDMYI VPLFDAS ITTGRMSRREVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {	t RRANQAGVTRADRDNVRTVDSFLMHPPKRVFKRLFIDEGLMLHTGCVNFLTLISQCD1}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAB82441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="RNA replicase protein"
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FGPMFSELTRMLLERVDTSKFLFYTRKTPTQIEEFFSDLDSSQAMEILELDISKYDKS
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AYVYGDTQQIPFICRVANFPYPKHFARLVVDEKEDRRITLRCPADVTFFLNKKYDGSV
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SLTYDIGGNFAAHLFKGRDYVHCCMPNLDVRDIARHEGHKEAVHGYISRLKRQRRPVP
EYQRAAFNNYSENPHFVHCDQPFQQCALSTVNGDDTYAIALHSVYDIPVEEFGSALLR
                                                                                                                                                                                                                                                                                                                                                             codon_start=1
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REFERENCE
AUTHORS
TITLE
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AUTHORS
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SOURCE
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VERSION
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AF254924
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Best Local S
Matches 139
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MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5475 GTTGACAATTTCAGGAAAAAGAAAAGGAAGATTGGAGGAAGGGATGTGATTAGTAAGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5415 GTTGAGGGTTTCGAAGGTGTAGTTGACGAATTCATCGATTCGGTTGCAGCATTTAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AAGTACAGACCGGAGAAGTACGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAGAAA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribgrass mosaic virus
Ribgrass mosaic virus
Viruses; ssRNA positive-strand viruses,
1 (bases 1 to 6301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-APR-2000) Dept. of Microbiology, 220, Han-Dan Road, Shanghai 200433, P.R. China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhu,H., Hong,J., Chen,J. and Yu,S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhu,H., Hong,J., Ye,R., Chen,J., Yu,S. and Adams,M.J. Sequence analysis shows that ribgrass mosaic virus Shanghai isolate (RMV-Sh) is closely related to Youcai mosaic virus Arch. Virol. 146 (6), 1231-1238 (2001)
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KNYKICYAAFHENMLLDCDSVTLEDIGATFQRAGDKLNFFFNHESTLNYHSFSNI
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VNKDFVYTVLNHIKTYQAKALTYYANTUSFVESIRSRVIINGVTARSEMPIDKATLFBFL
AMTFFLYTKLSHVQDEIVLKKFQKFDATAKELIWSSLCDALKGVIPSVKETLARGGFV
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VRQQFSNLLSAIVTPNQRFPETGYRVYVNSAVLKPLYEALMKSFDTRNRIIETEEESR
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                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic RNA"
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/db_xref="taxon:51680"
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                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Ribgrass mosaic virus"
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  55.0%;
illarity 72.4%;
Conservative
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GETYEKTAIVRLTATPLEIISRASPHVLVALTRHTTRCKYYTVVLDPMVNVISELGKL
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AMIKRIMNAPDLTGTIDIEDTASLVVEKFWDAYVYKEFSGTDGAMTRESFSKYLSKQ
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QNEFHCAVEYKIWEKLGIDEWLAEVWRQGHRKTTLKDYTAGIKTCLMYQRKSGDVTTF
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SICDIDLLVNVPLDKYRYVGYLGVAFTGEWLYPDFYKGGYTVSYIDKRLENSRESNIG
IYRAAKKDRFQFKLVPNYEVSTADAKRKPWQVHVRIQNLKIEAGWDPLALELYVSYAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKTLTACCRDGEPPEPTAKVYLVDGVPGCGKTKEILEKVNFSEDLVLVPGKEASKMII
RRANQAGVTRADKDNVRTVDSFLMHPPKRVFKRLFIDEGLMLHTGCVNFLTLLSHCDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEGLSLSNNAPFPCVSNLKEGLVPACGLGPKGANFDRVDMDISEFHLKSVDAVKKGAM
MSAVYTGKIKVQQMKNYVDYLSASLSATVSNLCKVLRDVHGVDPESQEKSGVMDVRRG
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RKKYGYFCGRYVIHHDRGAIVYYDPLKLISKLGCKHIRDEVHLEELRRSLCDVTSNLN
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AVVYGDTQQIPFICRVANFPYPSHFAKLVVDEKEDRRVTLRCPADVTYFLNTRYDGSV
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LKTLTACCRDGEPPEPTAKVVLVDGVPGCGKTKEILEKVNFSEDLVLVPGKEASKMII
                                                                                                                                                                                                                                                                                                                                                                                                             KYRYRPERYAGPDSLQYKEENGLQHHELESVPVFRSDVGRAHSDA"
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MSAVYTGKIKVQQMKNYVDXLSASLSATVSNLCKVLRDVHGVDPESQEKSGVMDVRRG
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  Score 103.4; DB 14;
Pred. No. 3.3e-17;
0; Mismatches 51;
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                                             Length 6301;
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Ribgrass
AF187045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-SEP-1999) Dept. of N
220 Handan Road, Shanghai 200433,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 798)
Zhu,H.Q., Ye,R., Xu,L., Hong,J., Chen,J.P.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribgrass mosaic virus
Ribgrass mosaic virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhu,H.Q., Ye,R., Xu,L., Hong,J., Chen,J.P. and Yu,S.Q. The movement protein gene of ribgrass mosaic virus isc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
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                                                                            GTCGAAGGTTTCGAAGGTGTGGTTGACGATTTCGTCGATTCGGTTGCTGCATTCAAGGCG.
              TATAAGTACAGACCGGAGAAGTACGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAGA
                                                          GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG 60
TATAGATATAGACCGGAGAGATACGCCGGTCCTGATTCGTTACAATATAAAGAAGAAAAT 723
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$\franslation="MSYEPKVSDFLALTKKEEILPKALTRLKTVSISTKDVISVKESE
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\text{TYRANAKDRRFQFKLVPNYFVSTADAKKFVAIDSFRKKKKKIGGRDVN
\text{VTNNYVVKGLEEKVIAVNDPNYEGFEGVVDDVVDSVAAFKAIDSFRKKKKKIGGRDVN
\nnkyryrperyagddslQykeenglQhhelesvPvfrsdvgrahsda"
\text{131 c} 215 g 220 t
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                                                                                                                                                                                                                                                                                                                                                  /product="movement protein"
/protein_id="AAF01245.1"
/db_xref="GI:6010767"
                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                            /isolate="Shanghai"
/specific_host="Brassica chinensis"
/db_xref="taxon:51680"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Ribgrass mosaic
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                            country="China:Shanghai"
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Pred. No. 9.8e
0; Mismatches
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ismatches 51;
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Search completed: September 26, 2003, 09:38:54
Job time: 3216 secs
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Best Local Similarity 73.0
Matches 130; Conservative
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Naito,S.

Direct Submission

Submitted (29-SEP-1994) Satoshi Naito, Hokkaido University, Faculty Submitted (29-SEP-1994) Satoshi Naito, Hokkaido University, Faculty of Agriculture, Department of Applied Bioscience; Kita-9, Nishi-9, Kita-ku, Sapporo, Hokkaido 060, Japan Kita-ku, Sapporo, Hokkaido 060, Japan (E-mail:naito@Al.hines.hokudai.ac.jp, Tel:81-11-706-2800,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIVCG 6303 bp RNA linear Youcai mosaic virus genomic RNA, complete sequence. D38444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete nucleotide sequence of the genomic RNA of tobacco mosaic virus strain Cg
Virus Genes 16 (2), 173-176 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Youcai mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D38444.1 GI:556527
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Vamanaka,T., Komatani,H., Meshi,T., Naito,S., Ishikawa,M. and
                                                                                                                                                                      1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 6303)
                                                                                                                                                                                                                                                                                                        /organism="Youcal mosaic virus"
/mol_type="genomic RNA"
/strain="crucifer strain Cg"
/db_xref="taxon:228578"
1178 c 1568 g 1747 t
                                                                                                                                                                                                                                                    47.9%;
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Pred. No. 1.3e-13; 
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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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| SIDSI_gcgdata/geneseq/geneseqn-embl/Na1980.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:
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Clone TXS.GFP-HIRE
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ecre	AAF45092		2128		38.6	24	ი
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Hormone-like prote	AAV01704		759	O		21	
Arabidopsis thali	ABX60706		327	0	9	20	
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IRES element IRES	AAL49136		152	78.7	4	9	

ALIGNMENTS

ABQ76058 standard; DNA; 188 BP

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WPI; 2002-557829/59
                                   Santa-Cruz S, Pogue GP,
                                                                            09-JAN-2001; 2001US-0758962.
                                                                                              09-JAN-2002; 2002WO-US01123.
                                                                                                                                                                                     IRES; internal ribosome entry site; viral protein; bicistronic; virus infection; coat protein; protein replacement therapy; crop;
                                                                                                                                                                                                                  Clone TXS.GFP-IRESs-CP containing IRES DNA sequence
                                                                                                                                                                                                                                       30-SEP-2002 (first entry)
                                                       (BIOS-) BIOSOURCE GENETICS CORP.
                                                                                                                                       WO200255719-A2
                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                              ABQ76058;
                                                                                                                   18-JUL-2002.
                                                                                                                                                                              value; seed oil content; ds
                                   Toth RL,
                                   Chapman
                               'n
                                  Carr
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New polypeptides contained in plant virus expression vectors, as gene

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AC ABQ7
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                                                    09-JAN-2002; 2002WO-US01123
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                                                                                                                                                                                                                                                                                                         30-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                              ABQ76062 standard; DNA; 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             construct comprising a bicistronic message with an intervening IRES. The constructs are used in a method for regulating the rate at which a virus infection spreads in a host. Regulation is achieved by placing the nucleic acid construct comprising an internal ribosomes entry site upstream of a coat protein gene, where the IRES is chosen by the rate of infection of the viral vector on a host in the presence of that IRES. The polynucleotide and vectors of the invention are useful for directing rapid and high-level expression of foreign genes in mature, differentiated, plant tissue. These are particularly useful in protein replacement therapy, or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter the oil content of the seed. This sequence represents a fragment of the clone TXS.GFT.IRESS-CP containing an IRES region described in the method of the invention.
                                                                                        18-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression tools, in protein replacement therapy or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      frame (ORF1) encoding a peptide and an ORF2 encoding a viral protein, where the IRES is located between ORF1 and ORF2. The novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant potato virus X-based viral vector containing a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel isolated polynucleotide comprising internal ribosome entry site (IRES) nucleotide sequence, an open rea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGTACAGACCGGAGAAGTACGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAGAAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACCATGG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGTACAGACCGGAGAAGTACGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAGAAGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 A; 26 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 188; DB 24; Pred. No. 7.7e-44; ; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are used in the construction of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                              bicistronic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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This invention describes a novel isolated polynucleotide comprising an CC internal ribosome entry site (IRES) nucleotide sequence, an open reading CC frame (ORF1) encoding a peptide and an ORF2 encoding a viral protein, CC where the IRES is located between ORF1 and ORF2. The novel polynucleotides of the invention are used in the construction of a crecombinant potato virus x-based viral vector containing a nucleic acid cc construct comprising a bicistronic message with an intervening IRES. The CC constructs are used in a method for regulating the rate at which a virus constructs are used in a method for regulating the rate at which a virus construct comprising an internal ribosomes entry site cupstream of a coat protein gene, where the IRES is chosen by the rate of infection of the viral vector on a host in the presence of that IRES. The CC infection of the viral vector on a host in the presence of that IRES. The CC infection of the viral vector on a host in the presence of that IRES. The CC infection of the viral vector of foreign genes in mature, compiled and high-level expression of foreign genes in mature, containing an internal value of a crop or alter the oil content of the seed. This sequence represents a fragment of the clone TXS.GFP.IRESS-CP cc containing an IRESCP region described in the method of the invention.
Query Match
Best Local
                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides contained in plant virus expression vectors, as gene expression tools, in protein replacement therapy or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Fig 4; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Santa-Cruz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOS-) BIOSOURCE GENETICS CORP.
                                                                        181
                                                                     BP; 64 A; 24 C; 49 G; 44 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pogue GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seeds
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                  Length 181;
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181 C 181
                    181 C
                                        121 · AAGTACAGACCGGAGAAGTACGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAGAGCT
                                                                                  61
                                                                                                                                                                   al Similarity
181; Conserv
                                                                                                      61
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                                                                                                                       GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG
                                                                                GTTGACAACTTTAAAAGAAGGAAAAAGGTTGAAGAAAAGGGTGTAGTAAGTAAGTAT
                                                                                          AAGTACAGACCGGAGAAGTACGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAGAAGCT
                    181
                                                                                                                                                                96.3%;
llarity 100.0%;
Conservative (
                                                                                                                                                             0;
                                                                                                                                                                Score 181; DB 24;
; Pred. No. 7.3e-42;
0; Mismatches 0;
                                                                                                                                                                   Indels
                                                                                                                                                                 0,
                                                                                                                                                                Gaps
                                        180
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IRES; internal ribosome entry site; viral protein; bicistronic; virus infection; coat protein; protein replacement therapy; crop. nutritional value; seed oil content; ds.
                                                                                                          Clone SC197
                                                                                                                                    30-SEP-2002
                                                                                                                                                                                        ABQ76064 standard; DNA; 181
                                                                                                     containing IREScp DNA sequence
                                                                                                                                 (first entry)
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WO200255719-A2

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RESULT 4
ABQ76063
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Best Local
         Clone SC196 containing IREScp DNA sequence
                                                                                     ABQ76063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           construct comprising a bicistronic message with an intervening IRES. The constructs are used in a method for regulating the rate at which a virus infection spreads in a host. Regulation is achieved by placing the nucleic acid construct comprising an internal ribosomes entry site upstream of a coat protein gene, where the IRES is chosen by the rate of infection of the viral vector on a host in the presence of that IRES. The polynucleotide and vectors of the invention are useful for directing rapid and high-level expression of foreign genes in mature, differentiated, plant tissue. These are particularly useful in protein replacement therapy, or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter the oil content of the seed. This sequence represents a fragment of the clone SC197 containing an IRESCP region described in the method of the invention.
                                                   30-SEP-2002
                                                                                                                      ABQ76063 standard; DNA; 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel isolated polynucleotide comprising an internal ribosome entry site (IRES) nucleotide sequence, an open read frame (ORF1) encoding a peptide and an ORF2 encoding a viral protein, where the IRES is located between ORF1 and ORF2. The novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotides of the invention are used in the construction of a recombinant potato virus X-based viral vector containing a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptides contained in plant virus expression vectors, as gene expression tools, in protein replacement therapy or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Fig 4; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Santa-Cruz S, Pogue GP, Toth RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JAN-2002; 2002WO-US01123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171;
                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                    181 C 181
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                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                 C 181
                                                                                                                                                                                                                                                                                  AAGTACAGACCGGAGAAGTACGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAGAAGACCT 180
                                                                                                                                                                                                                                                                                                                                                         GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGCTGCAGCATTTAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 BP; 61 A; 28 C; 53 G; 39 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·87.8%;
94.5%;
                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 165; DB 24;
Pred. No. 2.5e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chapman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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reading
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internal ribosome entry site (IRES) nucleotide sequence, an open reading CC frame (ORF1) encoding a peptide and an ORF2 encoding a viral protein, CC where the IRES is located between ORF1 and ORF2. The novel CC polynucleotides of the invention are used in the construction of a CC recombinant potato virus X-based viral vector containing a nucleic acid CC construct comprising a bicistronic message with an intervening IRES. The CC constructs are used in a method for regulating the rate at which a virus infection spreads in a host. Regulation is achieved by placing the nucleic acid construct comprising an internal ribosomes entry site upstream of a coat protein gene, where the IRES is chosen by the rate of infection of the viral vector on a host in the presence of that IRES. The CC infection of the viral vector of the invention are useful for directing CC infection of the viral vectors of the invention are useful for directing CC rapid and high-level expression of foreign genes in mature, CC replacement therapy, or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter the oil content of the seed. This sequence represents a fragment of the clone SC196 containing an XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 169; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 180 BP; 60 A; 31 C; 52 G; 37 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptides contained in plant virus expression vectors, as gene expression tools, in protein replacement therapy or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel isolated polynucleotide comprising an internal ribosome entry site (IRES) nucleotide sequence, an open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 4; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the oil content of seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-557829/59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOS-) BIOSOURCE GENETICS CORP.
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180 C 180
                                                               181 C 181
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                                                                                                                                                                                                                                                                                                                                                                              GTCGACGGTATCGATAAGCCTGATATCGAACTCGCCGATTCGGGTGCTGCA-TTAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                               GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.5%; Score 151.4; DB 24; 93.4%; Pred. No. 1.8e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oil content; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 180;
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RESULT 5 ABQ76060/c ID ABQ76060 standard; DNA; 137

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                                                                                                                                                                                        Best Local Sir
Matches 153;
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                      Sequence 187 BP; 45 A; 47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel isolated polynucleotide comprising an internal ribosome entry site (IRES) nucleotide sequence, an open readiframe (ORF1) encoding a peptide and an ORF2 encoding a viral protein, where the IRES is located between ORF1 and ORF2. The novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides contained in plant virus expression vectors, as gene expression tools, in protein replacement therapy or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 3; 33pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Santa-Cruz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JAN-2002; 2002WO-US01123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the oil content of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOS-) BIOSOURCE GENETICS CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200255719-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ76060
                            149
                                                              120
                                                                                                                            180
60
                                                                                            9
                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              internal ribosome entry site; viral protein; bicistronic;
infection; coat protein; protein replacement therapy; crop;
                                                                                                                                                                                                       Similarity
               CTGATTCGTTTAATTTGAAAGAAGAAGAAGAGCTCACCAT 186
                                                                         AGGTTGAAGAAAAGGGTGTAGTAAGTAAGTATAAGTACAGACCGGAGAAGTACGCCGGTC
                                                                                                                     AATTCGTCGATTCGGTTGCAGCATTTAAAGCGGTTGACAACTTTAAAAGAAGGAAAAAGA
                                                       AGGTTGAAGAAAAGGGTGTAGTAAGTAAGTACAGACCGGAGAAGTACGCCGGTC
                                                                                                                                                      AATTCGTCGATTCGGTTGCAGCATTTAAAGCGGTTGACAACTTTAAAAGAAGAAAAGA 88
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pogue GP,
                                                                                                                                                                                                     79.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               containing IRES DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oil content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toth RL,
                                                                                                                                                                                          0
                                                                                                                                                                                      Score 150; DB 24;
Pred. No. 4.4e-33;
0; Mismatches 5;
                                                                                                                                                                                                                                                      27 G; 68 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chapman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carr
                                                                                                                                                                                                                      Length 187;
                                                                                                                                                                                      Indels
                                                                                                                                                                                      0;
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reading
                                                                                                                      121
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RESULT 6
ABQ76059
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                                                                                                                                                                                                                                                                                                         This invention describes a novel isolated polynucleotide comprising an CC internal ribosome entry site (IRES) nucleotide sequence, an open reading CC frame (ORF1) encoding a peptide and an ORF2 encoding a viral protein, CC where the IRES is located between ORF1 and ORF2. The novel CC polynucleotides of the invention are used in the construction of a CC recombinant potato virus x-based viral vector containing a nucleic acid CC construct comprising a bicistronic message with an intervening IRES. The CC infection spreads in a method for regulating the rate at which a virus CC infection spreads in a host. Regulation is achieved by placing the construct comprising an internal ribosomes entry site cupstream of a coat protein gene, where the IRES is chosen by the rate of infection of the viral vector on a host in the presence of that IRES. The CC infection of the viral vector on a host in the presence of that IRES. The CC infection of the viral vector on a host in the presence of that IRES. The CC polynucleotide and vectors of the invention are useful for directing CC rapid and high-level expression of foreign genes in mature, and the construction of the viral vector on a lost in the presence of the construction of the invention are useful in protein CC replacement therapy, or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter the oil content of the seed. This sequence represents a fragment of the clone TXS.GFP HIRES-CP containing an IRES region described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X S X
                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 149; Conserv
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides contained in plant virus expression vectors, as gene expression tools, in protein replacement therapy or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 3; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a metabolic pathway to in
the oil content of seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Santa-Cruz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JAN-2001; 2001US-0758962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nutritional value; seed oil content; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone TXS.GFP-HIRES-CP containing IRES DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOS-) BIOSOURCE GENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRES;
                                           157
                                                                                      87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                internal ribosome entry site; viral protein; bicistronic; infection; coat protein; protein replacement therapy; crop:
                                                        GAAGGTTGAAGAAAAGGGTGTAGTAAGTAAGTATAAGTACAGACCGGAGAAGTACGCCGG
TCCTGATTCGTTTAATTTGAAAGAAGAAA 175
                                      GAAGGTTGAAGAAAAAGGGTGTAGTAAGTAAGTATAAGTACAGACCGGAGAAGTACGCCGG
                                                                                                                                                 251
                                                                                                                          CGAATTCGTCGATTCGGTTGCAGCATTTAAAGCGGTTGACAACTTTAAAAGAAGGAAAAA
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pogue GP,
                                                                                                                                                                                                                                                                                                     72 A; 51 C; 76 G; 52 T; 0 other;
                                                                                                                                                                                                                                        79.3%;
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                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                   Score 149; DB 24; Pred. No. 9.1e-33;
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                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chapman
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                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                   Indels
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TCCTGATTCGTTTAATTTGAAAGAAGAAA 245

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ABZ57802
                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid construct, the interference of the immunoglobulin superfamily, interferent, a protein, a protein, a protein, an antipone, an antipone, a growth factor, a cell membrane protein, a differentiation factor, a hormone, an antipone, a cell membrane protein, a protein, a protein, a prown, a growth factor, a cell membrane protein, a growth factor, a cell membrane protein, a differentiation factor, a harmone, an antipone, a cell membrane protein, a differentiation factor, a hormone, an antipone, a cell membrane protein, a differentiation factor, a hormone, an antipone, a sell membrane protein, a differentiation factor, a harmone, and may be Arabidopsis, Barasica, maize, alfalfa, soybean, a maize, alfalfa, soybean, a maize, alfalfa, soybean, a content and antipone differentiation of a multimeric kinase (claimed).
                                                                                                                                                                                                                                                                                                                                                           Sequence 148 BP; 56 A; 17 C; 40 G; 35 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of complex proteins in plants. Nucleic acid constructs contain, from 5' to 3', a transcription initiator and a plurality of structural genes, each separated by an IRES. In a claimed nucleic acid construct, the IRES is IREScp148. Complex proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the nucleotide sequence of internal ribosome entry site IREScp148cr from the genome of the crucifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid constructs comprising a transcriptional regulatory element, first and second coding regions, and an internal ribosome entry site element, useful for transiently or stably expressing active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ribosome entry site IREScpl48cr from the genome of the crucifes tobacco mosaic virus. The invention relates to the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 10; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-167400/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-2002; 2002WO-US17927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2002101006-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Internal ribosome entry site; IRES; transgenic plant; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ICON-) ICON GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-2001; 2001US-297103P
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                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                         al Similarity
148; Conserv
         61
                                                             88
                                                                                                                                          28 GAATTCGTCGATTCGGTTGCAGCATTTAAAGCGGTTGACAACTTTAAAAGAAGGAAAAAG
                                                    AAGGTTGAAGAAAAGGGTGTAGTAAGTAAGTATAAGTACAGACCGGAGAAGTACGCCGGT 147
AAGGTTGAAGAAAAGGGTGTAGTAAGTAAGTACAGACCGGAGAAGTACGCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tobacco virus internal ribosome entry site IREScp148
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                          78.7%; 5-
100.0%; Pr
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                  cottonseed, sunflower or a legume.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bossie
                                                                                                                                                                                                                                                            Score 148; DB 25;
Pred. No. 1.5e-32;
                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                              Length 148;
                                                                                                                                                                                                                                      Indels
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120
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ABV75164
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                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                   plant a genomic nucleic acid construct comprising at least one internal ribosome entry site (IRES) in operable association with a reporter gene; and (b) detecting the expression of the reporter gene as an indication of insertion of the nucleic acid construct into a transcriptionally active region. The method for identifying and characterizing transcriptionally active regions in plants, is useful for producing transgenic plants and seeds, as is the method for introducing a nucleic acid into plants. The method is also useful for observing or measuring phenotype in an organism. The present sequence represents an IRES element derived from the genome of the crucifer tobacco mosaic virus (crTMV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying and characterizing transcriptionally active regions in plants, useful for producing transgenic plants, comprises inserting nucleic acid constructs (called landing pads) with internal ribosome entry site(s) into plant genes .
                                                                                                                                                                                                                                             Sequence 148
                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to identifying and characterizing tranactive regions in plants. The method involves (a) inserting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 17; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-067578/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tobacco mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-2003
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                            148
121
                                                                                                                                                                                   148;
                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 CCTGATTCGTTTAATTTGAAAGAAGAAA 175
                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CCTGATTCGTTTAATTTGAAAGAAGAAA 148
                                                                                                                        ᆫ
                                                                                                                                                                                                Similarity
                CCTGATTCGTTTAATTTGAAAGAAGAAA 175
                                                      AAGGTTGAAGAAAAGGGTGTAGTAAGTAAGTATAAGTACAGACCGGAGAAGTACGCCGGT
                                                                                                                     AAGGTTGAAGAAAAGGGTGTAGTAAGTAAGTATAAGTACAGACCGGAGAAGTACGCCGGT
                                                                                                                                                   GAATTCGTCGATTCGGTTGCAGCATTTAAAGCGGTTGACAACTTTAAAAGAAGGAAAAAG
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                           BP; 56 A; 17 C; 40 G; 35 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA; 148 BP.
                                                                                                                                                                                78.7%; Score 148; DB 25; 100.0%; Pred. No. 1.5e-32; tive .0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bossie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRES element IREScp148cr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry site; IRES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Petty TJ;
                                                                                                                                                                                                           Length 148;
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          transcriptionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic;
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ID AAL4
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Best Local S
Matches 113
                                                                                                                                                                                                                                                                                      The present invention relates to a method of controlling a selected blockemical process or cascade in a plant. This involves the introduction of a heterologous DNA sequence into the plant genome, and infection by a viral transfer vector containing a second heterologous sequence, which is able to cause the first sequence to be switched on. The method is used to produce selected gene products in transgenic plants, particularly pharmaceutical polypeptides but also sugars and biodegradable polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Controlling biochemical processes in plants, useful for producing e.g. pharmaceutical peptides, from interaction between components in genome and viral transfer vector
                                                                                                                                                                                                                                      Sequence 152 BP; 57
                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 20; 92pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klimyuk V, Benning G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-FEB-2001; 2001DE-1009354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ICON-) ICON GENETICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein production;
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                                                                                                                                                                                                                                                                   present sequence is an RNA sequence the invention.
                            148
 121
                                                           61
                                                                                     88
                                                                                                            al Similarity
113; Conserv
                        CCTGATTCGTTTAATTTGAAAGAAGAAA 175
                                                      AAGGUUGAAGAAAAGGGUGUAGUAAGUAAGUAUAAGUACAGACCGGAGAAGUACGCCGGU
                                                                      AAGGTTGAAGAAAAGGGTGTAGTAAGTAAGTATAAGTACAGACCGGAGAAGTACGCCCGT
CCUGAUUCGUUUAAUUUGAAAGAAGAAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001DE-1009354.
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102..127
/*tag- c
129..135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bound_moiety= "binds nucleotides 94-88 of itself"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tag-
                                                                                                                                                                                                                                   A; 17 C; 41 G; 37 U; 0 other;
                                                                                                                                                                         78.7%; Score 148; DB 24; 76.4%; Pred. No. 1.6e-32; tive 35; Mismatches 0;
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                                                                                                                                                                                                                                                                              described in
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                                                                                                                                                                                                       Length 152;
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AAX87568
ID AAX87
                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 133
                                                                                                                                                                                                                                                                                                                                                                                                                                 subgenomic promoter, coat protein open reading frame and 3' end. It was obtained by PCR amplification. The CDNA was used in the construction of a tobamoviral vector for expression of heterologous genes in Arabidopsis thaliana. The invention provides methods for rapidly determining the function of nucleic acid sequences by transfecting them into a host organism to effect expression, and analysing the resulting phenotypic and biochemical changes. Methods for silencing endogenous genes, for selecting desired functions of RNAs and proteins, and for inhibiting an endogenous
                                                                                                                                                                                                                                                                                                                                                                        Sequence 1543 BP; 433 A; 280 C; 396 G; 434 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the nucleotide sequence of a ribgrass mosaic virus fragment in vector plasmid KS+. The sequence includes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining the function of polynucleotide sequences and their encoded proteins by transfecting them into a host organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Della-Cioppa
Kumagai MH,
                                                                                                                                                                                                                                                                                                                                                                                                                      protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 12; Page 65-66; 156pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPT; 1999-458459/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribgrass mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribgrass mosaic virus cDNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX87568 standard; cDNA; 1543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIOS-) BIOSOURCE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene function; protein function; tobamovirus; coat protein; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-1998;
                                           777
                                                                                    118
                                                                                                                             717
                                                                                                                                                                                                                                                                                             133;
                                                                                                                                                             1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG,
                                                                                                                                                                                                                                                                                                            Similarity
                                                                           TATAAGTACAGACCGGAGAAGTACGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAGA 177
  GCTCACCA 185
                                         TATAGATATAGACCGGAGAGATACGCCGGTCCTGATTCGTTACAATATAAAGAAGAAAAT
                                                                                                                         GTCGAAGGTTTCGAAGGTGTGGTTGACGATTTCGTCGATTCGGTTGCTGCATTCAAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                 in a plant host are also provided
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G, Erwin RL, Fitzmaurice WP,
Lindbo JA, McGee DR, Padgett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                            47.28;
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                                                                                                                                                                                                                                                                                      Score 88.8; D
Pred. No. 1.5e
O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                            .5e-15
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HS, Pogue
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GGTTTACA 844

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                            and isoprenoid biosynthetic pathways and inactive gene sites (pseudogene). Genes of the invention are used to enhance blosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP) and isoprenoid pathway derived products in the plastids of transgenic plants and microalgae, for productny herbicide or antiblotic resistant transgenic plants and microalgae, for providing transformed cells with increased isoprenoid production compared to non-transformed cells, and for providing a cell with an inserted polynuclectide sequence encoding one or more products of interest. The present sequence is pBSNT27 vector containing Nicotiana tabacum chloroplast gene fragment. This vector is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HAHN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the use of specific genes of the mevalonate and isoprenoid biosynthetic pathways and inactive gene sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of specific genes of mevalonate and isoprenoid biosynthetic pathways, for providing a cell with herbicide or antibiotic resistance, and for providing transformed cells having increased isoprenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pBSNT27 vector containing N. tabacum chloroplast gene fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mevalonate; isopentenyl diphosphate; herbicide resistance; DMAPP; IPP; isoprenoid; dimethylallyl diphosphate; antibiotic resistance; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD30982;
                                                                                               5482
                                                                                                                                                                                                  5542
                                             121
                                                                                                                                                  2
                                                                                                                                                                                                                          1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTTCGGTTGCAGCATTTAAAGCG
                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAHN F M.
KUEHNLE A R.
                                                                                     TGGGTAGCTGTTAAACCGGGTCGAATACTTTATGAAATGGGTGGAGTAACAGAAAAT 5423
                                                                                                               GTCGACGGTATCGATAAGCTTGATATCGAATTCCTGCAGCCCGGGGGATCCCCTGAATAT 548:
                                                                                                                                                                                                                                                                                                                                                                                               6215 BP; 1667 A; 1396 C; 1268 G; 1884 T; 0 other;
                                          AAGTACAGACCGG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 100-103; 193pp; English
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-221703P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tobacco;
                                                                                                                                                                                                                                                                                                                       23.1%;
57.9%;
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                               Score 43.4; DB 24;
Pred. No. 0.015;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                            Length 6215;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                          0;
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AAD31038/c ID AAD31038 standard; DNA; 7252 BP.

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6520 60 0

GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG

TGGGTAGCTGTTGTTAAACCGGGTCGAATACTTTATGAAATGGGTGGAGTAACAGAAAAT

Query Match Best Local : Matches

Similarity 77; Conserv

Conservative

23.1%;

Score 43.4; DB pred. No. 0.015; 0; Mismatches

DB 24; 56;

Indels Length 7252;

0;

0 other;

Sequence 7252 BP; 1820 A; 1719 C; 1653 G; 2060 T;

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RESULT 12

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X P X P X O S O S X R R R R R X X D X D X A C
                                           C (pseudogene). Genes of the invention are used to enhance biosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP) and isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP) and isopentenyl daphosphate (IPP), dimethylallyl diphosphate (DMAPP) and isopentenyl daphosphate (IPP), dimethylallyl diphosphate (DMAPP) and isopentenyl darkway derived products of the providing transformed cells with a for providing transformed cells with an inserted polynucleotide sequence encoding one or more products of interest. The present sequence is plastid transformation vector pHKO7 containing operon C DNA which encodes the entire mevalonate pathway. This operon contains S. cerevisiae orfs encoding phosphomevalonate vinase (MMC), mevalonate kinase (MWK), mevalonate kinase (MWK), mevalonate diphosphate decarboxylase (MDD), acetoacetyl thiolase (AACT); A. thaliana orfs encoding 3-hydroxy-3-methylglutaryl-coenzyme A companies (MMG-CoA) synthase (MMGS), HMG-CoA reductase (HMGRT) and R. capsulatus
                                                                                                                                                                                                                                                                                                                                                     and
                                    orf encoding
                                                                                                                                                                                                                                                                                                                                                              The invention relates to the use of specific genes of the mevalonate
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of specific genes of mevalonate and isoprenoid biosynthetic pathways, for providing a cell with herbicide or antibiotic resistance, and for providing transformed cells having increased isoprenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-2000; 2000US-221703P
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Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isoprenoid; dimethylallyl diphosphate; antibiotic resistance; enzyme; transgenic plant; yeast; phosphomevalonate kinase; HMGRt; HMGS; AACT; mevalonate kinase; mevalonate kinase; HMG-CoA; MDD; acetoacetyl thiolase; 3-hydroxy-3-methylglutaryl-coenzyme A synthase; MYK; PMK; HMG-CoA reductase; IPP isomerase; IPPI; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KUEH/) KUEHNLE A R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plastid transformation vector pHKO7 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isoprenoid;
                                                                                                                                                                                                                                                                                                                                                 isoprenoid
                                                                                                                                                                                                                                                                                                                                                                                                         Page 169-173; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuehnle AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae. Arabidopsis thaliana. Rhodobacter capsulatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dimethylallyl diphosphate; antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isopentenyl diphosphate; herbicide resistance;
                                    IPP isomerase (IPPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                            biosynthetic pathways and inactive gene
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ATAGCCAGAAGGG 6447

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AAD31040/c
ID AAD31040 standard; DNA;
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                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                  The invention relates to the use of specific genes of the mevalonate and isoprenoid blosynthetic pathways and inactive gene sites (pseudogene). Genes of the invention are used to enhance blosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP) and isoprenoid pathway derived products in the plastids of transgenic plants and microalgae, for producting harbicide or antiblotic resistant transgenic plants and microalgae, for providing transformed cells with increased isoprenoid production compared to non-transformed cells, and for providing a cell with an inserted polynucleotide sequence encoding one or more products of interest. The present sequence is plastid transformation vector pHKO5 containing Rhodobacter capsulatus phytoene synthase (crtB) EC 2.5.1.32 encoding DNA.
                                                                                                                                                                                                                                         Sequence 7252 BP; 1820 A; 1719 C; 1653 G; 2060 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of specific genes of mevalonate and isoprenoid biosynthetic pathways, for providing a cell with herbicide or antibiotic resistance, and for providing transformed cells having increased isoprenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 89; Page 181-185; 193pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pHKO5 vector containing R. capsulatus phytoene synthase (crtB)
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                                                                                                                        6579
                                                                                          62
                                                                                                                                                                                 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KUEHNLE A R.
ATAGCCAGAAGGG 6447
                             AAGTACAGACCGG
                                                        TGGGTAGCTGTTGTTAAACCGGGTCGAATACTTTATGAAATGGGTGGAGTAACAGAAAAT
                                                                                   GTCGACGGTATCGATAAGCTTGATATCGAATTCCTGCAGCCCGGGGGATCCCCCTGAATAT
                                                                                                                                          GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuehnle AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant; phytoene synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isopentenyl diphosphate; herbicide resistance; DM/
dimethylallyl diphosphate; antibiotic resistance;
                                                                                                                                                                              23.1%; Score 43.4; DB 57.9%; Pred. No. 0.015; tive 0; Mismatches
                              133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7252
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                                                                                                                                                                                                            24;
                                                                                                                                                                                 56;
                                                                                                                                                                                                            Length 7252;
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                                                                                                                    6520
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61

Query Match Best Local S Matches 77

l Similarity 77; Conserv

Conservative

23.18; 57.98;

Score 43.4; DB 24; Pred. No. 0.017; 0; Mismatches 56;

Length 13917; Indels

0,

Gaps

0

13184 TGGGTAGCTGTTGATAAACCGGGTCGAATACTTTATGAAATGGGTGGAGTAACAGAAAAT 13125

Sequence

13917 BP;

3882 A; 2923 C; 3063 G; 4049 T; 0 other;

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RESULT 14
AAD31037/c
ID AAD31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the use of specific genes of the mevalonate can disoprenoid biosynthetic pathways and inactive gene sites (pseudogene), Genes of the invention are used to enhance biosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP) cand isoprenoid pathway derived products in the plastids of transgenic plants and microalgae, for producing herbicide or antibiotic resistant transgenic plants and microalgae, for providing transformed cells with increased isoprenoid production compared to non-transformed cells, and for providing a cell with an inserted polynucleotide sequence encoding one or more products of interest. The present sequence is plastid transformation vector pHKO4 containing operon B DNA which encodes the entire mevalonate pathway. This operon contains S. cerevisiae orfs encoding phosphomevalonate Kinase (PMK), mevalonate kinase (MKK), mevalonate kinase (MKK), the contains of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of specific genes of mevalonate and isoprenoid biosynthetic pathways, for providing a cell with herbicide or antibiotic resistance, and for providing transformed cells having increased isoprenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mevalonate; isopentenyl diphosphate; herbicide resistance; DMAPP; IPP isoprenoid; dimethylallyl diphosphate; antibiotic resistance; enzyme; transgenic plant; yeast; phosphomevalonate kinase; HMGRt; HMGS; AACT; mevalonate kinase; mevalonate diphosphate decarboxylase; HMG-COA; MDD acetoacetyl thiolase; 3-hydroxy-3-methylglutaryl-coenzyme A synthase; MYK; PMK; HMG-COA reductase; ds.
                                                               and A. thaliana orfs
(HMG-CoA) synthase (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2000; 2000US-221703P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Chimeric -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HAHN/) HAHN F M.
(KUEH/) KUEHNLE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200210398-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 161-168; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae. Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                           fs encoding 3-hydroxy-3-methylglutaryl-coenzyme
(HMGS) and HMG-COA reductase (HMGRt).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₿P.
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The invention relates to the isolation of genes AAC59624-C59669 encoding CC XX human secreted proteins AAB34439-B34484. The genes can be used to CC generate fusion proteins by linking to the gene for the human CC immunoglobulin G Fc portion (AAC59615) for increasing the stability of CC the fusion protein as compared to the human protein only. The genes and CC conditions, e.g. by protein or gene therapy. The genes are isolated CC conditions, e.g. by protein or gene therapy. The genes are isolated CC conditions, proteins, antibodies and (ant)agonists are useful in CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC cliesese, multiple sclerosis, rheumatoid arthritis and ulcerative CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial isohaemias; (d) condities; (e) neurological diseases e.g. cerebral anoxia and cepilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
AAC59625/c
ID AAC59625 standard; cDNA; 1456
   Query Match
Best Local Similarity
Matches 64; Conserv
                                                                                                                                Sequence 1456 BP; 411 A; 297 C; 295 G; 445 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Pages 314-315; 384p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-602216/57.
P-PSDB; AAB34440.
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08-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAR-2000; 2000WO-US06828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein cDNA sequence #2.
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   Conservative
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                                                                                                                                                                                                           infections.
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99US-0169616.
                                22.2%; Score 41.8; DB 21; 63.4%; Pred. No. 0.03;
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Mismatches
                                                            Length 1456
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1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG 60

Indels

0;

Gaps

₽₽ Search completed: September 26, 2003, 08:45:10 Job time: 282 secs 밁 Š å 1450 1390 GCCAACATTCTAAGGCAGAGCATAGATAAAGAAGATGGAAA 1350 61 GTTGACAACTTTAAAAGAAGGAAAAAGAAGGTTGAAGAAAA 101

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
  nucleic search, using sw model
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188
1 gtcgacggtatcga
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            569978 seqs, 220691566 residues
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US-09-422-2668-20
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US-08-928-928-798-2
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US-08-928-928-790A-2
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US-08-928-829-22
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(without alignments)
1257.273 Million cell updates/sec
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657 GTCGAAGGTTTCGAAGGTGTGG 61 GTTGACAACTTTAAAAGAAGA	133 133	OF INVENTION: TRAIT IN A DONOR PUT INVENTION: A DONOR PUT OF INVENTION: ORIENTATIO OF INVENTION: ORIENTATIO OF INVENTION: ORIENTATIO OF INVENTION NUMBER: US/ TY FILING DATE: 199-07-2 OF SEQ ID NOS: 42 OF SEQ ID NOS: 42 RE: FastSEQ for Windows NO 9 11 1543 DNA DNA USA TISM: Ribgrass mosaic viru	301A-9 9, Application US/09359 0. 6426185 INFORMATION: NT: Kumagai, Monto H. NT: della-Cioppa, Guy F. NT: Erwin, Robert L. NT: MCGee, David R.	35.4 18.8 7560 4 US. 35 18.6 2126 3 US. 34.8 18.5 858 4 US. 34.8 18.5 1840 3 US. 34.8 18.5 3810 4 US. 34.8 18.5 3810 4 US. 34.8 18.5 4434 3 US. 34.8 18.5 4432 3 US. 34.8 18.5 4432 3 US.
GTCGAAGGTTRCGAAGGTGTGGTTGACGATTTCGTCGATTCCGTTGCTGCATTCAAGGCG GTTGACAACTTTAAAAGAAGGAAAAAGAAGGTTGAAGGAAAAAGGTTGTAGTAAGTAAG [47.2%; Score 88.8; DB 4; Length 1543; imilarity 70.7%; Pred. No. 8.3e-18; Conservative 0; Mismatches 52; Indels 3; Gaps GTCGACGGTATCGATAAGCTTGATATCGATTCGGTTGCAGCATTTAAAGCG	TRANSFECTING A DIFFERENT HOST 1A	IGNMENTS	US-09-026-221-4 US-08-789-354-1 US-09-110-937-1 US-09-058-7258-1 US-09-232-857-1 US-09-232-857-1 US-09-904-615-30 US-09-643-597-91 US-09-480-8844-91 US-09-480-8844-91 US-09-480-642-6450-7 US-09-066-046-26 US-09-066-046-26 US-09-066-046-27 US-09-066-0450-71 US-09-462-6450-7 US-09-462-6450-7 US-09-462-6450-7 US-09-462-6450-7 US-09-462-6450-7 US-09-815-809-1 US-09-815-809-1 US-09-815-809-1 US-09-08-815-809-1 US-09-08-815-809-1 US-09-08-815-809-1 US-09-08-815-809-1 US-09-08-815-809-1 US-09-08-815-809-1
CTGCATTCAAGGCG 716 TAAGTAAGTAAG 117		NUCLEIC ACID SEQUENCE OF PLANT IN AN ANTI-SENSE		Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 30, Appli Sequence 91, Appli Sequence 12, Appli Sequence 12, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 15, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

RESULT 2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:

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                                                                                  GENERAL INFORMATION:
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                                                    APPLICANT: HINNEN, Albert
APPLICANT: HEGEMANN, Johannes
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TOPOLOGY: line
IMMEDIATE SOURCE:
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                20, Application US/09402266B
5, 6537767
                                                                                                                                                                                                                                                             74 AAAGAAGGAAAAAGGATTGAAGAAAAGGGTGTAGTAAGTAAGTATAAGTACAGACCGG
                                                                                                                                                                                                                                                                                                                 14 ATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCGGTTGACAACTTTA
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           HEGEMANN, Johannes
MUNDER, Thomas
SCHUSTER, Tilmer
FELDMANN, Horst
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; OTHER INFORMATION: Synthetic sequence
'US-09-402-2668-20
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                                                     Query Match
Best Local Similarity 78.9
----- 45; Conservative
                                                                                                                                                                                                     SEQ ID NO 3
LENGTH: 1094
TYPE: DNA
ORGANISM: Staphylococcus aureus
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Best Local (
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LENGTH: 4102
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EARLIER FILING DATE: 1997-09-25
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                                                                                                                                                                                                                                                                                                                                                                                                                           ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/EP98/01904
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: DE 19713572.2
PRIOR FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/402,266E CURRENT FILING DATE: 1999-10-08
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TITLE OF INVENTION: Process for Screening Antimycotically Active Substances
FILE REFERENCE: 38005-0094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                            tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                             ITLE OF INVENTION: Murf
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1062 GTCGACGGTATCGATAAGCTTGATATCGAATTCCTGCAGCCCGTCGCATTTTTCATA 1006
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5, 6287807
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78.9%;
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                                                                                     Score 37.8; DB Pred. No. 0.02;
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                                                                   Mismatches
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                                                                                                    Length 1094;
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RESULT 5 US-08-928-799A-4

Patent No. 60693

Application US/08928799A

GENERAL INFORMATION: APPLICANT: OSBOTO

Thomas C le, David

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RESULT 6
US-08:553-367A-5
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; LOCATION:
US-08-928-799A-4
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Best Local Similarity
                                                                                                                                                                                                                   Sequence 5, Application US/08553367A Patent No. 5939539
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Theodo
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           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER:
                                                          COUNTRY:
                                                                             STATE:
                                                                                     CITY: Washington
                                                                                                        STREET:
                                                                                                                    DDRESSEE:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                     BER OF SEQUENCES:
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LE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES
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EDNESS: double
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                                                                         D.C.
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                                                                                                     E: Wenderoth, Lind & Ponack, L.L.P. 2033 K Street, N.W., Suite 800
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           3.5 inch, 1.44 mb
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Appl
Patent No. 61980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,367
FILING DATE: NO. 6198021ember 27, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFORMATION FOR SEQ ID NO:
                                                                                                                  SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1490 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO
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                                                                                    FILING DATE:
                                                                                                   APPLICATION NUMBER:
                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                         STREET: 2033 K St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                             ITLE OF INVENTION:
                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                             ADDRESSEE:
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SOFTWARE: Wordperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
55; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CTCTCAAGAAAAAAAAAAAAAG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 AACTTTAAAAGAAGGAAAAAGAAG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 GGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCGGTTGAC 66
                                                                                                                                                                                                                   20006
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                                                                                                                                                                                                                                                D.C.
                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09295306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTATCGATAAGCTTGATATCGAATTCGAGGATCCGGGGACCATGGACAAAAACCCCCAAAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1490 base pairs
                                                                                                                                                                                                                                                                             E: Wenderoth, Lind & Ponack, L.L.P. 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                U.S.A.
                                                                                                                                                                                                                                                                                                                             Theodor LANGE et al.
VENTION: GA 20-OXIDASE GENE SEQUENCES
EQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                 IBM Compatible
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Pred. No. 0.025;
0; Mismatches
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NAME: Lee Cheng REGISTRATION NUMBER:

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US-09-734-719-5
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Patent No. 6455675
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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ANTI-SENSE: NO
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RELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
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REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 2000-1678/LC/01784
TELECOMMUNICATION INFORMATION:
                                                      ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CTCTCAAGAAAAAAAAAAGAAAAG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 AACTITAAAAGAAGGAAAAAGAAG 90
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                                                                                       APPLICATION NUMBER: 09/295,306
FILING DATE: April 21, 1999
APPLICATION NUMBER: 08/553,367
FILING DATE: NO. 6455675ember 27,
APPLICATION NUMBER: PCT/EEP4/01664
FILING DATE: May 24, 1994
                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/734,719
FILING DATE: 13-Dec-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WOrdperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTATCGATAAGCTTGATATCGAATTCGAGGATCCGGGACCATGGACAAAAACCCCCAAAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TY: Washington
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2033 K Street, N.W., Suite 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
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Best Local S
Matches 55
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GENERAL INFORMATION:
                                                    TELEX: 360619
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                        APPLICATION NUMBER: US/08/352,902D FILLING DATE: 09-Dec-1994 CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ADDITORMETAN
                                                                                                                                                                                                                                                                                                                                                                              ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (503) 224-6655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Arabidopsis thaliana IMMEDIATE SOURCE: CLONE: pAT2353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liskay, Robert M.
Bronner, C. Eric
Baker, Sean M.
Bollag, Roni J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 GGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCGGTTGAC 66
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Oregon
                                                                                                                TELEFAX: (503)
                                                                                                                                                                          REFERENCE/DOCKET NUMBER: OHSU 306B
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Portland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 520 S.W. Yamhill Street, Suite 200
LENGTH: 821 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kolisch, Hartwell, Dickinson, McCormack
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                                                                                                                  295-6679
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                                                                                     Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                  FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                 MOLECULE TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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                                                                      Local Similarity
                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1 Sou:
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLE OF INVENTION: Hybrid Spring Oilseed Brassica napus
                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                OCATION:
                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 LASSIFICATION:
                                                                                                                                                                                                                                                          RANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: Human Chromosome 7q
                       1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 GTCGACGGTATCGATAAGCTTGATATCGAATTCCTCGA 49
                                                         44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53703
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                                                                                                                                                                                                                                                                      nucleic acid
GTCGACGGCATCGATAAGCTTGATATCGAATTCCTGCAGTCTCATTCTACATGTGAA 79
                                                                                                                                                                                                                                                                                                                                                                                                    Berson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WI
                                                                                                                                                                        WG6B10.T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08928799A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 South Pinckney St
                                                                                                                                                                                                                                                                                                                                 608-251-9166
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                                                                                                                             primer_bind
146..165
                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quarles & Brady
                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                         double
                                                                                                                                                                                                                                                                                                                                                                                                 Bennett
                                                                     19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomas C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.48; 97.48;
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                                                                                                                                                                                                                                                                                                                                                                                   37094
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                                                                   Score 36.2; DB 3; Pred. No. 0.047;
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Pred. No. 0.048; ...
0; Mismatches 1;
                                                      Mismatches
                                                        13;
                                                                                 Length 474;
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                                                     Gaps
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NFORMATION FOR SEQ ID NO:
 NAME/KEY: CDS
LOCATION: 2.1191
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                  FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                  MOLECULE TYPE:
                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1638 base pair
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 40,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                    COPOLOGY:
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                                                                                                                                                                  1638 base pairs
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                                                                                                                  linear
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ENTION: A NO.
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Koziel, Michael G
Mullins, Martha A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
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Kostichka, N. Kristy
                                                                                                                                                                                                                                   919-541-8582
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                                                                                                   CDNA
                                                                                                                                                                                                                                                                                                                                   MBER: US 08/037,057
25-MAR-1993
                                                                                                                              single
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/product= "Translation of cDNA encoding VIP3A(a) receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                               US 08/314,594
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Query Match Best Local

Similarity

18.98;

Score 35.6; DB 2; Pred. No. 0.1; 0; Mismatches 24;

24; Indels

0

Gaps

Length 1638;

Conservative

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US-09-233-336A-8

Mismatches

Indels

0;

Gaps

B 24;

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09-233-336A-8/c
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                         STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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LOCATION: 2..1191
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                              POTHETICAL:
                                                                                                                                        LENGTH: 1638 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                          NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 09-SEP-1994
                                                NAME/KEY:
                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                   ELEPHONE:
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                                                                                                                                                                                                                                                                                                                 DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 Skyline Drive
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Koziel, Michael G
Mullins, Martha A
                                               CDS
                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desai, Nalini M
Kostichka, N. Kristy
                                                                                                                                                                                                                    919-541-8582
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                                                                                                                                                                                                                                                                                 Gary
                                                                                                                                                                                                                                                                                                                                                           23-MAR-1994
                                                                                                                                                                                                                                                                                                            UMBER: US 08/037,057
25-MAR-1993
                                                                                            CDNA
                                                                                                                        single
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/product= "Translation of cDNA encoding VIP3A(a) receptor"
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US-09-233-752A-8/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                    TELEPHONE: 919-541-859
TELEFAX: 919-541-8689
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 23-MAR-
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                               TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FITLE OF INVENTION:
                                                                                                                                                                                                                             RIOR APPLICATION DATA:
                                                                                                                                  NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30B
                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 25-MA
                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/314,594
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1573 CTTATAAATTTTTA 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8, Application US/09233752A
p. 6137033
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                          nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hawthorne
                          1638 base pairs
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7 Skyline Drive
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Koziel, Michael G
Mullins, Martha A
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Duck, Nicholas B
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                                                                                                                                                                                            UMBER: US 08/037,057
25-MAR-1993
                                                                                                                                                                                                                                                                                          09-SEP-1994
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                                                                                                                                   CGC 1925
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US-09-233-752A-8
                                                                       Query Match
Best Local Similarity
                                                            Matches
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Best Local Similarity
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                                                                                                                          LOCATION: (2)..(1189)
OTHER INFORMATION: Translation of cDNA encoding VIP3A(a) receptor
OTHER INFORMATION: from Black cutworm
                                                                                                                                                                                                                                    Q ID NO 8
LENGTH: 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             equence 8, Application US/09402036
atent No. 6291156
                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                            NAME/KEY: CDS
                                                                                                                                                                                                                                                                                  MBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 2..1191
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                                                                                                                         NISM: Agrotis ipsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF INVENTION: FIG.
61 GTTGACAACTTTAA 74
|| || || |
1573 CTTATAAATTTTTA 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PELICATION NUMBER: PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/402,036 FILING DATE: 2000-02-08
                                                            50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG 60
                                                                                                                                                                                                                                                                                                             LICATION NUMBER:
                         GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG 60
                                                                                                                                                                                                                                                                   PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                     CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATION NUMBER: 08/838,219
G DATE: 1997-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Warren, Gregory W. Desai, Nalini Koziel, Michael
                                                                                                                                                                                                                                                                                                                                          ATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yu, Cao-Guo
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TION NUMBER:
                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant Pest Control
                                                                                                                                                                                                                                                                                                                                                        994-09-09
                                                                       18.9%; Score 35.6; 67.6%; Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Translation of cDNA encoding VIP3A(a) receptor"
                                                                                                                                                                                                                                                                                                                                                                                               08/463,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT/EP98/01952
                                                                                                                                                                                                                                                                                                            08/037,057
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                                                                                                                                                                                                                                                                                                                                        08/218,018
                                                                                                                                                                                                                                                                                                                                                                    08/314,594
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                                                           Mismatches
                                                                                    DB 3; Length 1638;
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NAME/KEY: CDS

LOCATION: (2)..(1189)

OTHER INFORMATION: Translation of cDNA encoding VIP3A(a) receptor

OTHER INFORMATION: from Black cutworm

US-09-904-226-8
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                                                                                                                                 Query Match
Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/904,226
                                                                                                                                                                                                                                                                                            ORGANISM: Agrotis ipsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/EP98/01952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPLICANT: Estruch, Juan J.
RPLICANT: Warren, Gregory W.
RPLICANT: Desai, Nalini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/838,219
FILING DATE: 1997-04-03
APPLICATION NUMBER: 08/832,263
1573 CTTATAAATTTTTA 1560
                                                               APPLICATION NUMBER: 08/463,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1573 CTTATAAATTTTTA 1560
                    61 GTTGACAACTTTAA 74
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PELICATION NUMBER: 08/832,265
ILING DATE: 1997-04-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                  PLICATION NUMBER:
LING DATE: 1994-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLICATION NUMBER: 08/314,594
LING DATE: 1994-09-09
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                                                                                              1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG 60
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                                                                                                                                 Conservative
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                                                                                                                                 0,
                                                                                                                                              Score 35.6; DB 4;
Pred. No. 0.1;
                                                                                                                                 Mismatches
                                                                                                                                 24;
                                                                                                                                                              Length 1638;
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Search completed: September 26, 2003, 10:16:57 Job time : 67 secs

Gaps

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
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Perfect score:
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188
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2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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US-09-758-962-5

US-09-758-962-7

US-09-758-962-3

US-09-758-962-3

US-09-758-962-2

US-10-155-420-2

US-10-211-079-19

US-10-356-708-18

US-10-356-708-23

US-10-356-708-22

US-10-356-508-17

US-10-356-508-17

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US-10-133-934-9
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/US09C_PUBCOMB.seq:*
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30.0	36.6	36.6	36.6	36.6	37	37.4	37.4	37.8	37.8	37.8	38	38	38	38.4	. 38.4	39	39.2	39.8	40.2	43.4	43.4	43.4	43.4	81	88.8	88.8	88.8	88.8
19.5	19.5		19.5							20.1	20.2	20.2	20.2	20.4	20.4	20.7	20.9	21.2	21.4	23.1	23.1	23.1	23.1	٠	47.2	٠	٠	47.2
148	148	148	148	148	4941	458	319	1094	587	122	616	465	434	781	382	456	327.	418	526	13917	7252	7252	6215	1536	1543	1543	1543	1543
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0S-10-052-942-152	ப	US-09-987-456-3	US-09-822-250-7	US-08-935-377-7	US-10-001-189-53	US-09-814-353-13302	US-09-814-353-13335	US-09-932-418-3	US-10-144-929-35	US-09-758-962-4	US-09-776-724A-62	-09-924-035A-	US-09-924-035A-656	US-10-198-846-4407	US-09-924-035A-720	US-09-814-353-15014	US-09-924-035A-52	US-09-924-035A-634	US-09-924-035A-430	-918-7	-918-74	-918-7	US-09-918-740-17	US-10-072-438-31	97	US-10-146-337-23	US-10-137-765-23	ÚS-10-120-630-9
Sequence 152, App		ω ,	7	`		_		Sequence 3, Appli	ω 5	4	٠	730	656		720,	1501	52	634		72,	75	73.	Sequence 17, Appl	31		23	23	Sequence 9, Appli

ALIGNMENTS

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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 188
TYPE: DNA
ORGANIZM: Potato virus
US-09-758-962-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-758-962-1
                                                                                                                                                                        Query Match
Best Local S
.Matches 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION TITLE OF INVENTION: FOREIGN GENES FROM PLANT VIRUS VECTEILE REFERENCE: 008010192NPUS00 CURRENT APPLICATION NUMBER: US/09/758,962 CURRENT FILING DATE: 2001-01-09
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SANTA CRUZ, SIMON APPLICANT: TOTH, RACHAEL L.
               188;
                                                          61
                                                                                     61
                                                                                                                                                                                    Similarity
                                                    GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG
AAGTACAGACCGGAGAAGTACGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                      TOTH, RACHAEL L
CHAPMAN, SEAN
CARR, FIONA
POGUE, GREGORY
                                                                                                                                                                      Conservative
                                                                                                                                                                   100.0%; Score 188; DB 11; 100.0%; Pred. No. 1.6e-43; tive 0; Mismatches 0;
                                                                                                                                                                     Indels
                                                                                                                                                                                                Length 188;
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 180
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                                                                                 120
                                                                                                                                        60
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181

CACCATGG 188

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NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Win
SEO ID NO 7
LENGTH: 181
TYPE: DNA
ORGANISM: Potato virus
US-09-758-962-7
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; ORGANISM: Potato virus
US-09-758-962-5
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CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 181
    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                     TITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION TITLE OF INVENTION: FOREIGN GENES FROM PLANT VIRUS VECTOR REFERENCE: 0008010192NPUS00 CURRENT APPLICATION NUMBER: US/09/758,962 CURRENT FILING DATE: 2001-01-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION OF TITLE OF INVENTION: FOREIGN GENES FROM PLANT VIRUS VECTOR: FILE REFERENCE: 008010192NUUS00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 96.3%; So Local Similarity 100.0%; I Local Similarity 100.0%; I see 181; Conservative 0;
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No. US20030049228A1
                                                                                                                                                                                                                      CARR, FIONA
POGUE, GREGO
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CHAPMAN, SEAN
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Pred. No. 1.4e-41;
 Score 165;
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 DB 11;
Length 181;
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RESULT 5
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US-09-758-962-6
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                                                Sequence 3, Application US/09758962 Publication No. US20030049228A1 GENERAL INFORMATION:
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Best Local Similarity 93.4%;
Matches 169; Conservative
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SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09758962
Publication No. US20030049228A1
APPLICANT: SANTA CRUZ, SIMON
APPLICANT: TOTH, RACHAEL L.
APPLICANT: CHAPMAN, SEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/758,962
CURRENT FILING DATE: 2001-01-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION OF INTERIOR FOREIGN GENES FROM PLANT VIRUS VECTORS FILE REFERENCE: 08010.192NpUS00
                                                                                                                                                         180 C
                                                                                                                                                                                        181 C 181
                                                                                                                                                                                                                      120 AAGTACAGACCGGCGAAGTGCGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAGAAGAGCT
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                                                                                                                                                                                                                                                                                                                                           1 GTCGACGGTATCGATAAGCCTGATATCGAACTCGCCGATTCGGGTGCTGCA-TTAAAGCG
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POGUE, GREGORY
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Pred. No. 3.2e-33;
0; Mismatches 11;
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0; Mismatches 10;
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RESULT 7
US-10-165-420-2
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CURRENT APPLICATION NUMBER: US/09/758,962
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 251
TYPE: DNA
ORGANISM: Potato virus
US-09-758-962-2
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; ORGANISM: Potato virus
US-09-758-962-3
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                                                                                                                                                                                                                                                                                                Query Match 79.3%; Score 149; DB 11; Best Local Similarity 100.0%; Pred. No. 1.7e-32;
                                                                                                                                                                                                                                                                                      Matches 149;
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Publication No. US20030049228A1
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Best Local Similarity 96.8%;
Matches 153; Conservative
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SEQ ID NO 3
LENGTH: 187
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CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 8
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TITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION OF
TITLE OF INVENTION: FOREIGN GENES FROM PLANT VIRUS VECTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: POGUE, GREGORY
ITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION OF
ITLE OF INVENTION: FOREIGN GENES FROM PLANT VIRUS VECTORS
                                                                                     147 TCCTGATTCGTTTAATTTGAAAGAAGAAGAAA 175
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                                                                  TCCTGATTCGTTTAATTTGAAAGAAGAAA 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAPMAN, SEAN
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Pred. No. 8e-33;
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PRIOR APPLICATION NUMBER: US 10/098,155

PRIOR FILING DATE: 2002-03-14

NUMBER OF SEQ ID NOS: 29

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 19

LENGTH: 796

TYPE: DNA

ORGANISM: tobamovirus

US-10-211-079-19
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US-10-211-079-19
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; OTHER INFORMATION: CTTMV
US-10-165-420-2
                                                                                                                         Matches
                                                                                                                                       Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/211,079 CURRENT FILING DATE: 2002-08-01
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                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Nucleic Acid Molecules Encoding CEL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Padgett, Hal S. APPLICANT: Vaewhongs, And
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TITLE OF INVENTION: PRODUCTION OF PROTEINS IN PLANTS
FILE REFERENCE: 57717 (11758)
                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: P-LG 5381
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TYPE: DNA
ORGANISM: Tobacco mosaic virus
                                    544 GTCGAAGGTTTCGAAGGCGTGGTTGACGATTCGTCGTCGCAGTCGCAGCATTCAAGGCG
                                                                                                                       130;
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148;
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                                                                       GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG
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Vojdani, Fakhrieh S.
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                                                                                                                       Conservative
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                                                                                                                                   47.9%; Score 90; DB 12; Length 796, 73.0%; Pred. No. 1.le-15;
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                                                                                                                     Mismatches
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                                                                                             PRIOR APPLICATION NUMBER: US 10/098,155
PRIOR FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FRASSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 799
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                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local :
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OTHER INFORMATION: synthetic construct-10-211-079-23
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ORGANISM: Tobamovirus
-10-356-708-18
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/211,079
CURRENT FILING DATE: 2002-08-01
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CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: 60/353,722
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 10/098,155
PRIOR APPLICATION NUMBER: 10/098,155
PRIOR FILING DATE: 2002-03-14
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;EQ ID NO 18
LENGTH: 796
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                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                TYPE: DNA
                                                                                                                                                                                                                                                       ITLE OF INVENTION: Nucleic Acid Molecules Encoding CELITLE OF INVENTION: Endonuclease and Methods of Use The ILE REFERENCE: P-LG 5381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         544 GTCGAAGGTTTCGAAGGCGTGGTTGACGATTTCGTCGATTCGGTCGCAGCATTCAAGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG
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Vojdani, Fakhrieh S.
Smith, Mark L.
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No. US20030148315A1
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73.0%;
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Pred. No. 1.1e-15;
0; Mismatches 45
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US-10-211-079-22
; Sequence 22, Application US/10211079
; Publication No. US20030148315A1
; GENERAL INFORMATION:
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US-10-356-708-22
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Best Local Similarity
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LENGTH: 799
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                                     APPLICANT: Padgett, Hal S. APPLICANT: Vaewhongs, And
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 10/098,155
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 10/211,079
PRIOR FILING DATE: 2002-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/356,708
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: 60/353,722
PRIOR FILING DATE: 2000-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence derived from tomato mosaic virus and TMV-Cg
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Vojdani, Fakhrieh S.
Smith, Mark L.
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Pred. No. 1.1e-15;
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Pred. No. 1.1e-15;
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APPLICANT:

INVENTION:

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Best Local Similarity
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Best Local Similarity 73.0
Matches 130; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/356,708
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: 60/353,722
PRIOR FILING DATE: 2000-02-01
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                                                                                                                                                                                                                                                                                                                                                        LENGTH: 80
TYPE: DNA
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NUMBER OF SEQ ID NOS: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: P-LG 10100
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CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 10/098,155
PRIOR FILING DATE: 2002-03-14
                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: This sequence was derived by shuffling in accordance with the me OTHER INFORMATION: hodogy of the present invention.
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 10/098,155
FILING DATE: 2002-03-14
APPLICATION NUMBER: 10/211,079
118 TATAAGTACAGACCGGAGAAGTACGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAA 175
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                                                                         GTCGAAGGTTTCGAAGGCGTGGTTGACGATTTCGTCGATTCGGTCGCAGCATTCAAGGCG 615
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73.0%;
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Pred. No. 1.1e-15;
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; TYPE: DNA
; ORGANISM: Ribgrass mosaic virus (RMV)
US-10-236-508-17
                                  SEQ ID NO 9
LENGTH: 15.
TYPE: DNA
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TITLE OF INVENTION:
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Best Local Similarity
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                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/133,934
CURRENT FILING DATE: 2002-04-24
                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                          PRIOR APPLICATION NUMBER: US/09/359,301A PRIOR FILING DATE: 1999-07-21
                                                                                                                                                                                                                                                                                      APPLICANT: Kumagai, Monto H.
APPLICANT: della-Cioppa, Guy R.
APPLICANT: Erwin Robert L.
APPLICANT: McGee, David R.
ORGANISM: Ribgrass
LO-133-934-9
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CURRENT FILING DATE: 2002-09-06
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                                                   1543
                                                                                                                                                                                                           INVENTION: METHOD OF DETERMINING THE PRESENCE OF A INVENTION: TRAIT IN A PLANT BY TRANSFECTING A NUCLEIC ACID SEQUENCE OF INVENTION: A DOWOR PLANT INTO A DIFFERENT HOST PLANT IN AN ANTI-SENSE INVENTION: ORIENTATION
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Robert L. Erwin
David R. McGee
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                 mosaic virus
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                                                                                      Windows Version 3.0
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70.78;
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Pred. No. 3e-15;
Pred. No. 3e-15;
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PLANT INTO
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Query Match 47.2%; Score 88.8; DB 14; Lei Best Local Similarity 70.7%; pred No 35-15.	9 14; Length 1543;		
Matches 133; Conservative 0; Mismatches 52; Indels	Indels	3; Gaps	1;
Y 1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG	CGATTCGGTTGCAGCATT		60
b 657 GTCGAAGGTTTCGAAGGTGTGGTTGACGATTCGTCGATTCGGTTGCTTCAAGGCG 716	CGATTCGGTTGCTGCATTC	CAAGGCG .	716
9 61 GTTGACAACTTTAAAAGAAGGAAAAAGAAGGTTGAAGAAAAGGGTGTAGTAAGTAA	AGAAAAGGGTGTAGT	MAGTAAG	117
D 717 ATTGACAGTTTCCGAAAGAAAAAGAATTGGAGGAAGGGATGTAAATAATAATA	 ;AGGAAGGGATGTAAATAAT	FAATAAG	776
Y 118 TATAAGTACAGACCGGAGAAGTACGCCGGTCCTGATTCGTTTAATTTGAAAGAAGAAAGA	TTCGTTTAATTTGAAAGAA	AGAAAGA	177
777 TATAGATATAGACCGGAGAGATACGCCGGTCCTGATTCGTTACAATATAAAGAAGAAAAT 836	TTCGTTACAATATAAAGAA	AGAAAAT 8	836
y 178 GCTCACCA 185			
b 837 GGTTTACA 844			
earch completed: September 26, 2003, 10:21:22 ob time : 257 secs		•	

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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                       Score
     47.6
44.8
44.2
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Match Length DB ID
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188
1 gtcgacggtatcgataagct.....gaagaaagagctcaccatgg 188
     25.3
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CH1#002_H	s2-164	BAC05		JAAAEH02	SJAAAFB08	AACG05	AEG09	2 6280	#025_C	#001_C	#003 A	00440	AME07	602699	#002 G	7h08.x	#001 H	#002 B	191-60	602769	602700	602700	602700	602700	2 3728	182-164	*000	S.TMASD10	1 600	F 002 F	291-60_	381-60_	ADDO8	AJG10	:92-164	KYE602702	٠,	٦٥	

ALIGNMENTS

	COMMENT	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	rocus	RESULT 1 BU745631
Contact: George AL Division of Genetic Medicine vanderbilt University 529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA 7e1: 615 936 2660 Fax: 615 936 2661 Email: al.george@vanderbilt.edu Email: al.george@vanderbilt.edu Insert Length: 1622 Std Error: 0.00 Seq primer: T3: ATTAACCCTCACTAAAGGGA High quality sequence start: 59	Other_ESTs: CH2#001_B09T7	Expressed sequence tags from Canine heart	Yi,Y., Desai,R., Olarte,M., Henthorn,P. and George A.L.	1 (bases 1 to 775)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canida	Canis familiaris	Canis familiaris (dog)	EST.	BU745631.1 GI:23695092	BU745631	Canis familiaris cDNA clone CH2#001_B09 3', mRNA sequence.	B09T3 Canine heart normalized cDNA Library 1	BU745631 775 bp mRNA linear EST 10-OCT-2002	

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BASE COUNT
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AUTHORS
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                                                                                                                                                                                                                                                 Contact: Zeguang Han
Chinese National Human
351 Guo Shoujing Road,
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                Schistosoma japonicum
Schistosoma japonicum
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                                                                                                                                                                                                                                                                                                                      Expressed sequence tags from male adults of Schistosoma japonicum
                                                                                                                                                                                                                                                                                                                                                 Hu,W., Yan,Q., Shen,D., Liu,F., Xu,X., Zhu,Z., Zhang,X., Wang,J., Sub,J., Xu,X., Wang,Z., Zeng,L., Rong,Y., Wu,X., Qu,J., Xu,Z., Huang,J., Ma,Y., Wang,S., Wang,Z., Xue,C., Feng,Z., Chen,Z. and Han
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':
                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma. 1 (bases 1 to 687)
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Location/Qualifiers
                                                                                                                                                                                                      hanzg@chgc.sh.cn
                              /tissue_type="Whole body"
/dev_stage="adult"
/lab_host="rabbits"
/clone_lib="SJM"
a 135 c 125 g 234 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: heart; Vector: pBluescript; Site_1: 5' of vector Not1; Site_2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed" a 135 g 249 t
                                                                                                                      /organism-"Schistosoma
/mol_type-"mRNA"
/db_xref-"taxon:6182"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="mixed developmental stages (adult, 30 day -day fetal)"
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/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CH2#001_B09"
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                                      61 GTTGACAACTTTAAAAGAAGGAAAAAGAAGGTTGAAGAAAA 101
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                                                                                                 1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG
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Adelson,D.L. and Gill,C.A.
Bovine ESTs (Adelson and Gill)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB169414 790 bp mRNA KYE602702101.R1 CSEQFXL23 stomach-abomasum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: david.adelson@tamu.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 9798452616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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GTTGACATTTTCCACAACAGGTGTTAGAATGTTGAAAAAAA 104
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                                                                                                                                                                                                                                                  /tissue_type="stomach-abomasum"
/clone_lib="csmcpxt23 stomach-abomasum"
/clone_lib="csmcpxt23 stomach-abomasum; Vector: psluescript sk+;
/note="forgan: stomach-abomasum; Vector: psluescript sk+;
Site_1: Not1; Site_2: EcoRI; sequence 5' of the insert
(5'-NNN . ..NNInsert)
GCGAATTGGAGTCCACCGCGGTGGCCGGCCTCGAG. Sequence 3' of
the inserts (AAGAATTGGATATCAAGCTTATCGATACCGTCGACCTCGAG.
non-normalized library, sequenced 3' with M13R primer."
a 149 c 174 g 256 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
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Pred. No. 9.4;
O; Mismatches
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Pred. No. 7.2;
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                                                                    BU791304
SJFAGG07
BU791304
Schistosoma japonicum
Schistosoma japonicum
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                                                   BU791304.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raghavan, N., Miler, A.N., Gardner, M., FitzGerald, P.C., Kerlavage ,A.R., Johnston, D.A., Lewis, F.A. and Knight, M. Comparative gene analysis of Biomphalaria glabrata hemocytes preand post-exposure to miracidia of Schistosoma mansoni Mol. Blochem. Parasitol. 126 (2), 181-191 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomedical Research Institute
12111 Parklawn Dr., Rockville,
Tel: 301-881-3300 ext.128
Fax: 301-770-4756
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW740521 254 bp mRNA linear EST 27
BRII0478 Biomphalaria glabrata (BS-90) unexposed Lambda 28
Biomphalaria glabrata cDNA clone RBGIG26TR, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Raghavan N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Lymnaeoidea; Planorbidae; Biomphalaria. 1 (bases 1 to 254)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomphalaria glabrata (bloodfluke planorb)
Biomphalaria glabrata
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AW740521
                                                                                                                                                                                          CAAGTAACGTCCGCAACACAGCGC 111
                                                                                                                                                                                                                                                             GAGTTACATCCACATAACAGCGGTATTGAAAGTCCAAGACGATTAGTTACAGAGTAATCA
                                                                                                                                                                                                                             TAAGTACAGACCGGAGAAGTACGC 143
                                                                                                                                                                                                                                                                                                                               GTCGACGGTATCGATAAGCTTGATATCGAATTCGGCACGAGCTCGTGCCGAATTCGGCAC
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Location/Qualifiers
                                                                                      SJF Schistosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unexposed Biomphalaria glabrata (BS-90) snails and first strand cDNA synthesized using an oligo-dT primer-linker (XhoI). Second strand synthesis was followed by the ligation of EcoRI adaptors. Following digestion with xhoI, the completed, directional cDNA was cloned into Uni-ZAP XR Phagemid vector by Stratgene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescript SK-; Site_1: EcoRI; Sit
XhoI; Total RNA was isolated from the hemocytes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Biomphalaria glabrata (BS-90)-unexposed Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="hermaphrodite"
/cell_type="Hemocyte"
/lab_host="Laboratory host"
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'clone="RBGIG26TR"
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/strain-"BS-90"
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                                                     GI:28348311
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RESULT 6
BZ571990
 FEATURES
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KEYWORDS
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Best Local S
Matches 92
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                                                                                                                                                                                                                              AUTHORS
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                                                                                                                                     Psedomonas aeruginosa library J. Bacteriol., (2002) In precontact: Chris K. Raymond
                                                                                                                                                                                   Spencer, D.H., Raymond, C.K., Smith, E.E., Burns, J.L., Kaul, R. and Olsen, M.V. Whole-Genome-Sequence variation among mu
                                              Tel: 2062216954
Fax: 2066857244
                                                                                 University of Washington
Box 352145, Seattle, WA 98105-2145,
                  Class: shotgun
                             Email: craymond@u.washington.edu
                                                                                                                        Genome Center
                                                                                                                                                                                                                                                                 Pseudomonadaceae;
                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCGG
                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: hanzg@chgc.sh.cn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hu,W., Yan,Q., Shen,D., Liu,F., Xu,X., Zhu,Z., Zhang,X., Wang,J., Sun,J., Xu,X., Wang,Z., Zeng,L., Rong,Y., Wu,X., Qu,J., Xu,Z., Huang,J., Ma,Y., Wang,S., Wang,Z., Xue,C., Feng,Z., Chen,Z. and Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Zeguang
Chinese National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed sequence tags from female adults of Schistosoma japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
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                                                                                                                                                                                                                                               (bases 1 to 1017)
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a 112 c 101 g
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:6182"
/sex="female"
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                                                                                                                                                                                                                                                             Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43.4;
Pred. No. 14;
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BASE COUNT
ORIGIN
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AUTHORS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: al.george@vanderbilt.edu
Insert Length: 2104 Std Error: 0.00
Seg primer: T3: ATTAACCCTCACTAAAGGGA
                                                                                                                                                                                                                                                                                                                        Fax:
                                                                                                                                                                                                                                                                                                                                            Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville,
                                                                                                                                                                                                                                                                                                                                                                          Division of Genetic Medicine
                                                                                                                                                                                                                                                                                                                                                                                                   Other_ESTs: CH2#002_F04T7
                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed sequence tags from
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Y1,Y., Desai,R., Ola
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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        shepherd, pointer, oligo-dT primed*
a 266 c 271 g
                                            /note="Organ: heart; Vector: pBluescript; Site_1: 5' of vector Not1; Site_2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     library."
a 324 c
                                                                                                                                                                                                                                                                                                                                                                                         George AL
                                                                                                 pBluescript"
                                                                                                                             day retal)"
                                                                                                                                                    /clone="CH2#002_F04"
/tissue_type="heart"
/cell_type="heart"
                                                                                                                                                                                        /organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
                                                                                                                                    dev_stage="mixed developmental stages (adult, 30 day -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cione="msh2_2193"
/clone_lib="msh"
/note="Environmental
                                                                                                          'clone_lib="Canine heart normalized cDNA Library
                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain-"MSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
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ce tags from Canine heart
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26 GTCGACGGTATCGATAAGCTTGATATCGAATTCTTTTTTTGGAATGCAACAACTTTATTG
BZ561465 1092 bp DNA linear pacs2-164_3275.x4 pacs2-164 Pseudomonas aeruginosa pacs2-164_3275, genomic survey sequence.
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Adelson,D.L. and Gill,C.A.
Bovine ESTS (Adelson and Gill)
Unpublished
Contact: David L. Adelson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Animal Breeding and Genetics Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Boxidae; Boxid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: david.adelson@tamu.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 9798452616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Animal Science Dept., TAMU-2471,
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/mol_type="mRNA"
/db_xref="taxon:9913"
/db_xref="taxon:9913"
/tissue_type="stomach-abomasum"
/clone_lib="CSEQFXL/3 stomach-abomasum"
/note="Organ: stomach-abomasum; Vector: pBluescript
/note="Organ: stomach-abomasum; Vector: pBluescript
/site_1: Not1; Site_2: EcoRI; sequence 5' of the inse
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                             Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922
                                                                                                                                        Expressed sequence tags from female adults of Schistosoma japonicum Unpublished
                                                                                                                                                                                  Hu,W., Yan,Q., Shen,D., Liu,F., Xu,X., Zhu,Z., Zhang,X., Wang,J., Sun,J., Xu,X., Wang,Z., Zeng,L., Rong,Y., Wu,X., Qu,J., Xu,Z., Huang,J., Ma,Y., Wang,S., Wang,Z., Xue,C., Feng,Z., Chen,Z. and Han
                                                                                                                                                                                                                      Schistosoma japonicum Schistosoma japonicum Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Etrigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma. 1 (bases 1 to 269)

1. "" "" Chan D Liu.F. Xu.X., Zhu,Z., Zhang,X., Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTTAAAGCG 60
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SJFAJG10 SJF Schistosoma
BU802512
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GSS.
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Whole-Genome-Sequence variation among multiple isolates of Psedomonas acruginosa library
T Bactorial (1908) 1-1-1-1
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Location/Qualifiers
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/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
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Schistosoma japonicum
Schistosoma japonicum
Schistosoma japonicum
Eukaryota, Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 270)
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Chinese National Human
351 Guo Shoujing Road,
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expressed sequence tags from female adults of Schistosoma japonicum Unpublished
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SJFADD08 SJF Schistosoma
                                                                                                                                                                                                                                                                                                                                                 Email: hanzg@chgc.sh.cn.
                                                                                                                                                                                                                                                                                                                                                            Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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                                                                                                                                                                               /tissue_type="Whole body"
/dev_stage="adult"
/lab_host="rabbits"
/clone_lib="SJF"
a 47 c 42 g 94 t
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/dev_stage="adult".
/lab_host="rabbits"
/clone_lib="SJF"
a 47 c 42 g 93 t
                                                                                                                                                                                                                                                      /organism="Schistosoma
/mol_type="mRNA"
/db_xref="taxon:6182"
/sex="female"
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/mol_type="mRNA"
/db_xref="taxon:6182"
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                  Spencer, D.H., Raymond, C.K., Smith, E.E., Burns, J.L., Kaul, R. and Olsen, M.V. Whole-Genome-Sequence variation among mupsedomonas aeruginosa library
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                                                                                                                                                                                                   BZ549869 708 bp DNA linear GSS 17-DEC pacs1-60_2384.x1 pacs1-60 Pseudomonas aeruginosa genomic clone pacs1-60_2384, genomic survey sequence.
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                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                 Pseudomonas aeruginosa
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Box 352145, Seattle, WA 98105-2145, USA
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/note="clinical isolate 1-60 Whole genomic shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="1-60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Pseudomonas aeruginosa"
/mol_type-"genomic DNA"
                                                                                     1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42.8;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 g
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                                                                                                               Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB
                                   multiple isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
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                                                                 Sims, E.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                             GSS 17-DEC-2002
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SOURCE
ORGANISM
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BU744514
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ORIGIN
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Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                        TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GTTGACAACTTTAAAA 76
                                                                                                                                                                                       Division of Genetic Medicine Vanderbilt University 529 Light Hall, 2215 Garland Tel: 615 936 2660 Fax: 615 936 2661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BU744514 833 bp mRNA linear EST 10-O CH1#002_F10T3 Canine heart non-normalized cDNA Library in pBluescript Canis familiaris cDNA clone CH1#002_F10 3', mRNA
                                                                                                                                                         High quality sequence start: 65 High quality sequence stop: 656
                                                                                                                                                                                                                                                                                                                                    Other_ESTs: CH1#002_F10T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (dog)
Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55
                                                                                                                                                                                                                                                                                                                        Contact: George AL
                                                                                                                                                                                                                                                                                                                                                                    Expressed sequence tags from
                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 833)
Y1,Y., Desai,R., Ol
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BU744514.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
BU744514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chris K. Raymon
Genome Center
University of Washington
Box 352145, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                          /organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CHH#002_F10"
/tissue_type="heart"
/cell_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chris K. Raymond
'dev_stage="mixed developmental stages (adult, 30 day -
lay fetal)"
                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="pacs1-60_2384"
/clone_lib="pacs1-60"
/note="clinical isolate 1-60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="1-60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'db_xref="taxon:287"
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                                                                                                                                                                                                                                                                      2215 Garland Avenue,
                                                                                                                                                                                                                                                                                                                                                                                     Olarte, M.,
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Pred. No. 23;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      Canine heart
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                                                                                                                                                                                                                                                                                                                                                                                   George A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi; Canis.
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BASE COUNT
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AUTHORS.
TITLE
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BU745422
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SOURCE
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VERSION
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ORIGIN
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GTTGACAACTTTAAAAGAAGGAAAAAGAAGGTTGAAGAAA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                             Email: al.george@vanderbilt.edu
Insert Length: 1378 Std Error: 0.00
Seq primer: T3: ATTAACCCTCACTAAAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BU745422 958 bp mRNA linear EST 10-0 CH1#009_F03T3 Canine heart non-normalized cDNA Library in pBluescript Canis familiaris cDNA clone CH1#009_F03 3', mRNA
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529 Light Hall, 2215 Garland Avenue, Nashville,
Tel: 615 936 2660
Fax: 615 936 2661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Division of Genetic Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other_ESTs: CH1#009_F03T7
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
1 (bases 1 to 958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (dog)
Canis familiaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed sequence tags from
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                    310
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                                                                                                                                                                                                                                                                                                                                                                                            quality sequence start: 90 quality sequence stop: 759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Desai, R.,
                                                                                                                                                                                                                               /db_xref="taxon:9615"
/clone="CH1#009_F03"
/tlssue_type="heart"
/cell_type="heart"
        oligo-dT primed"
208 c
                                                                                      vector NotI; Site_2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left
                                                                                          dog heart (adult,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligo-dT primed'
175 c 222
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dog heart (adult, 30 day - 40 day fetal), right and left
atria and ventricle. Dog breed - mixed (beagle, German
                                                                                                                                'note="Organ: heart; Vector: pBluescript; Site_1: 5' of
                                                                                                                                                                                                                                                                                                               /organism="Canis familiaris"
/mol_type="mRNA"
                                                                                                                                                                   clone_lib="Canine heart non-normalized cDNA Library in
                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Canine heart non-normalized cDNA Library in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="Organ: heart; Vector: pBluescript;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.6%;
                                                                                                                                                                                                        stage="mixed developmental stages (adult, 30 day -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olarte,M., Henthorn,P. and George A.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42.4; DB 13; Pred. No. 22; 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TN 37232-0275, USA
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                                                                        German
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Best Local S
Matches 70
115 TTTGACAAGTTTCACTTAGCGCAATACACCTAAAAGGAAATCACGATACAAGGAAA 170
                     55 GTCGACGGTATCGATAAGCTTGATATCGAATTCTTTTTTTGGTTTTTAAAAGAAGATTTA 114
                                                                1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTGGGTTGCAGCATTTAAAGCG 60
                                                                                                                   Similarity
                                                                                                        Conservative
                                                                                                                 22.6%;
                                                                                                                  Score 42.4;
Pred. No. 22
                                                                                                       Mismatches
                                                                                                                                 DB 13;
                                                                                                       46;
                                                                                                                                Length 958;
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Search completed: September 26, Job time: 2204 secs 2003, 10:15:44

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